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STIC-Biotech/ChemLib

77633

From: Li, Ruixiang
Sent: Wednesday, October 09, 2002 4:50 PM
To: STIC-Biotech/ChemLib
Subject: Sequence search of Application NO:09/924,125

Please do a standard search on SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li
GAU 1646
CM1 10D19
Mail Box 10C01
306-0282

RECEIVED
OCT 10 2002
STIC

Point of Contact
P. Sheppard
Telephone number: (703) 308-4499
Searcher: _____
Phone: _____
Location: _____
Date Picked Up: _____
Date Completed: 10/12/02
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
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Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:45:54 : Search time 33 Seconds
(without alignments)
1120.836 Million cell updates/sec

Title: US-09-924-125-2
Perfect score: 1731
Sequence: 1 MNTVMQGFNRSEKPRDTR.....KTTASSQENHSSQTDNITLG 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_032802:*

1:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT:*
2:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT:*
3:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1982.DAT:*
4:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1983.DAT:*
5:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1984.DAT:*
6:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1985.DAT:*
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19:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1998.DAT:*
20:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA1999.DAT:*
21:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2000.DAT:*
22:	/SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	333	21	AAB23029 Human chemokine re
2	1731	100.0	333	22	AAB74397 Human G protein co
3	1731	100.0	333	22	AAB74494 Novel human G prot
4	1725	99.7	333	20	AAV02171 Human 7-transmembr
5	1725	99.7	333	21	AAV71299 Human orphan G pro
6	1725	99.7	333	21	AAB02833 Human G protein co
7	1725	99.7	333	22	AAU10588 Human HNEAA81 poly
8	1725	99.7	333	22	AAB31580 Amino acid sequenc
9	1710	98.8	333	22	AAE02494 Human CON203 G pro
10	1697	98.0	333	19	AAW77322 Human chemokine re
11	1402.5	81.0	336	22	AAB62472 Rat 7-transmembran

12	1372	79.3	337	22	AAB73484 Mouse G protein-co
13	1098.5	63.5	293	17	AAW04246 Human G-protein co
14	1098.5	63.5	293	21	AAB15412 Human G-protein co
15	1098.5	63.5	293	21	AAV67355 Human G-protein co
16	829	47.9	342	20	AAW81576 EBV-induced G-prot
17	829	47.9	342	21	AAV71306 Human orphan G pro
18	829	47.9	342	21	AAB02840 Human G protein co
19	829	47.9	342	21	AAV94444 Human 15625 recept
20	829	47.9	342	22	AAV79249 Human protein SEQ
21	829	47.9	342	22	AAE04386 Human P2-purinergr
22	828	47.8	342	21	AAV94445 Macaque ortholog o
23	816	47.1	315	22	AAE04385 Human P2-purinergr
24	807	46.6	343	22	AAE04384 Rat P2-purinergric
25	799	46.2	387	21	AAV94498 Rat MP-10 receptor
26	777	44.9	338	21	AAV58237 Human KIAA0001 rec
27	777	44.9	338	22	AAE04388 Human UDP-glucose
28	770.5	44.5	338	21	AAV97541 Rat KIAA0001 prote
29	767.5	44.3	338	21	AAV94270 Mouse 7-transmembr
30	692.5	40.0	358	21	AAV45039 Human G-protein co
31	692.5	40.0	358	21	AAV44365 Human G-protein co
32	692.5	40.0	358	22	AAE03199 Human G-protein co
33	692.5	40.0	358	22	AAE02499 Human G-protein co
34	692.5	40.0	358	22	AAB96884 Human novel G-prot
35	692.5	40.0	358	22	AAB83014 Human G-protein co
36	692.5	40.0	358	22	AAB94659 Human protein sequ
37	692.5	40.0	358	22	AAB67484 Amino acid sequenc
38	692.5	40.0	358	22	AAB85890 Human C-PLACE10032
39	685.5	39.6	384	22	AAB84205 Amino acid sequenc
40	677.5	39.1	358	20	AAV28280 Human G-protein co
41	674.5	39.0	358	22	AAE04387 Human G-protein co
42	584.5	33.8	267	22	AAE04387 Human P2-purinergr
43	556	32.1	132	20	AAV12278 Human 5' EST secre
44	505.5	29.2	319	19	AAW69735 Human C5a-like pro
45	505.5	29.2	319	19	AAW53896 Human G-protein co

ALIGNMENTS

RESULT 1
AAB23029 AAB23029 standard; Protein; 333 AA.

16-JAN-2001 (first entry)

Human chemokine receptor-like protein, SECX 2777610.

SECX protein; human; secreted; membrane-associated; cancer;
proliferation regulator; differentiation regulator; non-malignant tumour;
immune disorder; autoimmune disease; transplant rejection; allergy; AIDS;
infection; inflammatory disorder; arthritis; haematopoietic disorder;
skin disorder; cardiovascular disorder; atherosclerosis; restenosis;
neurological disease; Alzheimer's disease; trauma; wound;
spinal cord injury; skeletal disorder; cytostatic; immunosuppressive;
anti-HIV; antiinflammatory; antiarthritic; antiarteriosclerotic;
neuroprotective; vulnery; antiallergic; antimicrobial; cardiant;
dermatological; gene therapy.

OS Homo sapiens.
XX WO2000053742-A2.
PN
XX
PD 14-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06280.
XX
PR 09-MAR-1999; 99US-0123667.
XX 08-MAR-2000; 2000US-0123667.
PA
XX (CURA-) CURAGEN CORP.

PI Shinkets RA;
XX
DR WPI; 2000-594318/56.
DR N-PSDB; AAA93616.
XX
PT Novel human membrane associated or secreted polypeptides and
PT polynucleotides useful for diagnosis, prevention and treatment of
PT pathological states such as cancer, immune, cardiovascular and
PT neurological disorders
XX
PS Claim 1; Fig 1; 151pp; English.

CC Sequences AAB23029-B23048 represent human SECX proteins. The SECX
CC proteins of the invention are either secreted or membrane-associated
CC proteins and act as regulator of cellular proliferation and
CC differentiation. SECX proteins or nucleotides are useful for diagnosing
CC the presence of, or predisposition to, a disease associated with altered
CC levels of SECX proteins and nucleotides. The SECX proteins are also
CC useful to screen compounds that modulate SECX activity or expression. The
CC interaction of a SECX protein with other cellular proteins may be useful
CC to modulate the activity of a partner protein, cellular proliferation,
CC cellular differentiation and cell survival. SECX nucleotides are useful
CC for the recombinant expression of SECX protein, and may be used to detect
CC SECX mRNA or genetic lesions in the SECX gene. They may also be used to
CC modulate SECX expression (e.g., using antisense oligonucleotides). SECX
CC nucleic acid sequences are also useful for identifying a cell or tissue
CC type in a biological sample, and in forensic biology. SECX primers or
CC probes are useful for detecting the presence of SECX nucleotides and for
CC screening tissue cultures for contamination. Diseases that may be treated
CC or prevented using SECX proteins or nucleotides include cancer (e.g.,
CC colorectal carcinoma, prostate cancer), benign tumours, immune disorders
CC (including autoimmune diseases, transplant rejection, allergies, AIDS),
CC infections, inflammatory disorders, arthritis, haematopoietic disorders,
CC skin disorders, cardiovascular disorders, atherosclerosis, restenosis,
CC neurological diseases (e.g., Alzheimer's disease), trauma (e.g.,
CC surgical or traumatic wounds, spinal cord injury), and skeletal
CC disorders.

XX Sequence 333 AA;

Query Match 100.0%; Score 1731; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.2e-173;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTVMQGFNRSERCPRDTRIVQVLPALYTVFVLGILNTLALMVFVHIPSSSTFIY 60
DB 1 MNTVMQGFNRSERCPRDTRIVQVLPALYTVFVLGILNTLALMVFVHIPSSSTFIY 60
61 LKNTLVADLIMTLMPLPKILSDSHLAPWQRAFCRSSVIFETMYVGIVLLGLIAFDR 120
61 LKNTLVADLIMTLMPLPKILSDSHLAPWQRAFCRSSVIFETMYVGIVLLGLIAFDR 120
QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQMVNNICQIFWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKKLEGKVFVVV 240
DB 181 GLKWHQMVNNICQIFWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKKLEGKVFVVV 240
QY 241 AVEFVCFAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
DB 241 AVEFVCFAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
QY 301 KKFTKLPKCMQGRKTTASSQENHSSQTDNITLG 333
DB 301 KKFTKLPKCMQGRKTTASSQENHSSQTDNITLG 333

RESULT 2
AAB74397
ID AAB74397 standard; Protein; 333 AA.
XX

AC AAB74397;
XX
DT 11-JUL-2001 (first entry)
XX
DE Human G protein coupling receptor.
XX
KW Human; G protein coupling receptor; CNS; central nervous system.
XX
OS Homo sapiens.
XX
PN JP2001054389-A.
XX
PD 27-FEB-2001.
XX
PF 17-AUG-1999; 99JP-0230777.
XX
PR 17-AUG-1999; 99JP-0230777.
XX
PA (YAMA) YAMANOUCHI PHARM CO LTD.
XX
DR WPI; 2001-321039/34.
DR N-PSDB; AAF87601.

PT A novel G protein coupling receptor.
XX
PS Claim 1; page 11; 14pp; Japanese.

CC The present invention relates to a novel G protein coupling
CC receptor, a gene encoding for the receptor family, a process for
CC preparation of the receptor family, an antibody to the receptor
CC family and a method for screening using the receptor. The invention may
CC be used for screening of agents expected to be useful for
CC prevention and treatment of central nervous system (CNS) diseases.
CC The present sequence the G protein coupling receptor.

XX Sequence 333 AA;

Query Match 100.0%; Score 1731; DB 22; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.2e-173;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTVMQGFNRSERCPRDTRIVQVLPALYTVFVLGILNTLALMVFVHIPSSSTFIY 60
DB 1 MNTVMQGFNRSERCPRDTRIVQVLPALYTVFVLGILNTLALMVFVHIPSSSTFIY 60
61 LKNTLVADLIMTLMPLPKILSDSHLAPWQRAFCRSSVIFETMYVGIVLLGLIAFDR 120
61 LKNTLVADLIMTLMPLPKILSDSHLAPWQRAFCRSSVIFETMYVGIVLLGLIAFDR 120
QY 121 FLKTIIRPLRNIFLKKPVFAKTVSIFWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
DB 121 FLKTIIRPLRNIFLKKPVFAKTVSIFWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQMVNNICQIFWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKKLEGKVFVVV 240
DB 181 GLKWHQMVNNICQIFWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKKLEGKVFVVV 240
QY 241 AVEFVCFAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
DB 241 AVEFVCFAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
QY 301 KKFTKLPKCMQGRKTTASSQENHSSQTDNITLG 333
DB 301 KKFTKLPKCMQGRKTTASSQENHSSQTDNITLG 333

RESULT 3
AAB74494
ID AAB74494 standard; Protein; 333 AA.
XX
AC AAB74494;
XX
DT 31-MAY-2001 (first entry)

```
XX Novel human G protein coupled receptor.
DE
XX
KW Human; G protein coupled receptor; central nervous system disease;
KW schizophrenia; Parkinson's disease.
OS Homo sapiens.
XX JP2001029083-A.
XX
XX 06-FEB-2001.
XX
XX 23-JUL-1999; 99JP-0209918.
XX
XX 23-JUL-1999; 99JP-0209918.
XX
XX (YAMA ) YAMANOUCHI PHARM CO LTD.
XX
XX WPI; 2001-221498/23.
XX N-PSDB; AAF81501.
XX
XX A new G protein coupled receptor -
XX
XX Example 1; Page 11; 14pp; Japanese.
XX
XX The present invention provides the protein and coding sequences for a
XX novel human G protein coupled receptor. This is useful in the
XX identification of treatments for central nervous system diseases such as
XX schizophrenia, Parkinson's disease and aches.
XX
XX Sequence 333 AA;
SQ
Query Match 100.0%; Score 1731; DB 22; Length 333;
Best Local Similarity 100.0%; Pred. No. 6.2e-173;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MNTTVMOGFNRSERCPDRTRIQVLVFPALYTVVFLTGILLNTLALMVFVHIPSSSTFIY 60
Db 1 MNTTVMOGFNRSERCPDRTRIQVLVFPALYTVVFLTGILLNTLALMVFVHIPSSSTFIY 60
QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIVLLGLIAFDR 120
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIVLLGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIWFLFFISLPMILSNKEATFSSVKKCASLKGPL 180
Db 121 FLKIIRPLRNIFLKKPVFAKTVSIFIWFLFFISLPMILSNKEATFSSVKKCASLKGPL 180
QY 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKAKVYDSYRKSCKDRKNNKLEGVYEVVY 240
Db 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKAKVYDSYRKSCKDRKNNKLEGVYEVVY 240
QY 241 AVEFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFIKETTLLFLAATNICMDPLIYIFLC 300
Db 241 AVEFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFIKETTLLFLAATNICMDPLIYIFLC 300
QY 301 KFTTEKLPQMGRKTTASSQENHSSQTDNITLG 333
Db 301 KFTTEKLPQMGRKTTASSQENHSSQTDNITLG 333
RESULT 4
ID AAY02171 standard; Protein; 333 AA.
XX
XX AAY02171;
XX
XX 07-JUL-1999 (first entry)
XX
XX Human 7-transmembrane receptor protein designated HNEA81.
XX
XX Human 7-transmembrane receptor; HNEA81; bacterial disease; asthma;
KW fungal disease; viral disease; HIV-1; HIV-2; cancer; anorexia;
DE
```

```
KW Parkinson's disease; hypertension; osteoporosis; myocardial infarction;
KW manic depression; schizophrenia; Gilles de la Tourette's syndrome.
XX
XX Homo sapiens.
XX EP913471-A2.
XX
XX 06-MAY-1999.
XX
XX 25-AUG-1998; 98EP-0306805.
XX
XX 23-OCT-1997; 97US-0956975.
XX
XX (SMIK ) SMITHKLINE BEECHAM CORP.
XX
XX Halsey WS, Sathé GM;
XX
XX WPI; 1999-256627/22.
XX N-PSDB; AAX35385.
XX
XX New human 7-transmembrane receptor useful for diagnosing and
XX treating diseases such as HIV infection, anorexia and schizophrenia
XX
XX Claim 11; Page 8; 20pp; English.
XX
XX The present sequence represents a human 7-transmembrane receptor,
XX designated HNEA81. The products may be used in the treatment of
XX diseases which involve altered expression of HNEA81. These
XX include bacterial, fungal, or viral diseases including those
XX caused by HIV-1 and HIV-2, cancers, anorexia, Parkinson's disease,
XX hypertension, osteoporosis, myocardial infarction, asthma,
XX manic depression, schizophrenia and Gilles de la Tourette's syndrome.
XX
XX Sequence 333 AA;
SQ
Query Match 99.7%; Score 1725; DB 20; Length 333;
Best Local Similarity 99.7%; Pred. No. 2.6e-172;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MNTTVMOGFNRSERCPDRTRIQVLVFPALYTVVFLTGILLNTLALMVFVHIPSSSTFIY 60
Db 1 MNTTVMOGFNRSERCPDRTRIQVLVFPALYTVVFLTGILLNTLALMVFVHIPSSSTFIY 60
QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIVLLGLIAFDR 120
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIVLLGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
Db 121 FLKIIRPLRNIFLKKPVFAKTVSIFIWFLFFISLPMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKAKVYDSYRKSCKDRKNNKLEGVYEVVY 240
Db 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKAKVYDSYRKSCKDRKNNKLEGVYEVVY 240
QY 241 AVEFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFIKETTLLFLAATNICMDPLIYIFLC 300
Db 241 AVEFVCFAPFHFARVPYTHSQTNNTKDCRLQNLFIKETTLLFLAATNICMDPLIYIFLC 300
QY 301 KFTTEKLPQMGRKTTASSQENHSSQTDNITLG 333
Db 301 KFTTEKLPQMGRKTTASSQENHSSQTDNITLG 333
RESULT 5
ID AAY71299 standard; Protein; 333 AA.
XX
XX AAY71299;
XX
XX 02-NOV-2000 (first entry)
XX
XX Human orphan G protein-coupled receptor hARE-1.
DE
```


XX Human; orphan G protein-coupled receptor; GPCR; hARE-1; drug screening;
KW transmembrane receptor; expressed sequence tag; EST; signal cascade.
XX
OS Homo sapiens.
XX
PN WO200031258-A2.
XX
PD 02-JUN-2000.
XX
PF 13-OCT-1999; 99WO-US23687.
XX
PR 20-NOV-1998; 98US-0109213.
PR 16-FEB-1999; 99US-0120416.
PR 26-FEB-1999; 99US-0121852.
PR 12-MAR-1999; 99US-0123946.
PR 12-MAR-1999; 99US-0123949.
PR 28-MAY-1999; 99US-0136436.
PR 28-MAY-1999; 99US-0136437.
PR 28-MAY-1999; 99US-0136439.
PR 28-MAY-1999; 99US-0136567.
PR 28-MAY-1999; 99US-0137127.
PR 28-MAY-1999; 99US-0137131.
PR 29-JUN-1999; 99US-0141448.
PR 29-SEP-1999; 99US-0156555.
PR 29-SEP-1999; 99US-0156633.
PR 29-SEP-1999; 99US-0156634.
PR 29-SEP-1999; 99US-0156653.
PR 01-OCT-1999; 99US-0157280.
PR 01-OCT-1999; 99US-0157281.
PR 01-OCT-1999; 99US-0157282.
PR 01-OCT-1999; 99US-0157293.
PR 01-OCT-1999; 99US-0157294.
PR 12-OCT-1999; 99US-0416760.
PR 12-OCT-1999; 99US-0417044.
XX
PA (AREN-) ARENA PHARM INC.
XX
PI Chen R, Dang HT, Llaw CW, Lin I;
XX
DR WPI; 2000-400068/34.
DR N-PSDB; AAD01126.
XX
XX
PT Novel human orphan G protein-coupled receptors and the encoding cDNAs
PT for use in the identification of G protein-coupled receptor agonists -
XX
PS Claim 34; Page 65-66; 102pp; English.
XX
XX The present amino acid sequence is the hARE-1, an endogenous human
XX orphan G protein-coupled receptor (GPCR), expressed in the spleen and
XX peripheral leucocytes. The hARE-1 cDNA was identified using EST
XX (expressed sequence tag) 1689643 as a probe.
XX The orphan GPCR of the invention, like all GPCRs has seven transmembrane
XX alpha helices with an extracellular N-terminus and an intracellular
XX C-terminus. However, no endogenous ligands has yet been identified for
XX the proteins of the invention. The orphan GPCRs may be used in the
XX identification of their endogenous ligands, and to screen potential GPCR
XX agonists and antagonists for use as pharmaceutical agents. The proteins
XX may also be used in the study of GPCR-mediated signalling cascades, and
XX to elucidate their precise role in normal and diseased human conditions.
XX Nucleic acid encoding human orphan GPCRs may be used for tissue
XX localisation expression analysis to provide information about their
XX function in healthy and pathological states.
XX
SQ Sequence 333 AA;

Query Match 99.7%; Score 1725; DB 21; Length 333;
Best Local Similarity 99.7%; Pred. No. 2.6e-172;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNTFVMOGFNRSEPCPRDTRIVOLVFPALYTVFLTGILNTIALMWFVHIPSSSTFIY 60
Db 1 MNTFVMOGFNRSEPCPRDTRIVOLVFPALYTVFLTGILNTIALMWFVHIPSSSTFIY 60

QY 61 LKNTLVADLINTLMLPFKILSDSHLAPWOLRAFCVCRSSVIFETMYGIVLLGLIAFDR 120
Db 61 LKNTLVADLINTLMLPFKILSDSHLAPWOLRAFCVCRSSVIFETMYGIVLLGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIFWFLFISLPNMLSNKEATPSSVYKCCASLKGPL 180
Db 121 FLKIIRPLRNIFLKKPVFAKTVSIFIFWFLFISLPNMLSNKEATPSSVYKCCASLKGPL 180
QY 181 GLKWHQMVNNICQIFWTVFILMLVEYVYIAKKVYDSYRKSCKDRKNNKLEGVFVVV 240
Db 181 GLKWHQMVNNICQIFWTVFILMLVEYVYIAKKVYDSYRKSCKDRKNNKLEGVFVVV 240
QY 241 AVFVCFAPFHFARVPYTHSQTNNKTDCLQNQLFIKETTFLAATNICMDPLIYIFLC 300
Db 241 AVFVCFAPFHFARVPYTHSQTNNKTDCLQNQLFIKETTFLAATNICMDPLIYIFLC 300
QY 301 KFTTEKLPDMOGRKTTASSQENHSSQTDNITLG 333
Db 301 KFTTEKLPDMOGRKTTASSQENHSSQTDNITLG 333

RESULT 6
AAB02833
ID AAB02833 standard; Protein; 333 AA.

AC AAB02833;
DT 22-AUG-2000 (first entry)

DE Human G protein coupled receptor hARE-1 protien SEQ ID NO:20.

KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
KW identification; agonist; screening; therapeutic; pharmaceutical;
KW mutant.

OS Homo sapiens.

PN WO200022131-A2.

PD 20-APR-2000.

PF 13-OCT-1999; 99WO-US24065.

PR 13-OCT-1998; 98US-0170496.

PR 12-NOV-1998; 98US-0108029.

PR 20-NOV-1998; 98US-0109213.

PR 27-NOV-1998; 98US-0110060.

PR 16-FEB-1999; 99US-0120416.

PR 26-FEB-1999; 99US-0121852.

PR 12-MAR-1999; 99US-0123944.

PR 12-MAR-1999; 99US-0123945.

PR 12-MAR-1999; 99US-0123946.

PR 12-MAR-1999; 99US-0123948.

PR 12-MAR-1999; 99US-0123949.

PR 12-MAR-1999; 99US-0123951.

PR 28-MAY-1999; 99US-0136436.

PR 28-MAY-1999; 99US-0136437.

PR 28-MAY-1999; 99US-0136439.

PR 28-MAY-1999; 99US-0137127.

PR 28-MAY-1999; 99US-0137131.

PR 28-MAY-1999; 99US-0137567.

PR 30-JUN-1999; 99US-0141448.

PR 27-AUG-1999; 99US-0151114.

PR 03-SEP-1999; 99US-0152524.

PR 29-SEP-1999; 99US-0156633.

PR 29-SEP-1999; 99US-0156555.

PR 29-SEP-1999; 99US-0156634.

(AREN-) ARENA PHARM INC.

PI Behan DP, Lehmann-Bruinsma K, Chalmers DT, Chen R, Dang HT;
PI Gore M, Llaw CW, Lin I, Lowitz K, White C;

XX WPI: 2000-317986/27.
DR N-PSDB; AAA46027.
XX
PT Non-endogenous, human G protein-coupled receptors for screening
PT receptor, inverse or partial agonists useful as therapeutic agents
XX
PS Example 1; Page 94-95; 187pp; English.
XX
CC The present invention describes transmembrane receptors, preferably
CC human G protein coupled receptors (GPCR), for which the endogenous
CC ligand is unknown (Orphan GPCR receptors). More specifically the present
CC invention relates to non-endogenous, constitutively activated versions
CC of a human GPCR. These non-endogenous human GPCRs can be useful for
CC the direct identification of candidate compounds as receptors agonists,
CC inverse agonists or partial agonists for use as pharmaceutical agents.
CC AAA46017 to AAA46126 and AAB02825 to AAB02859 represent sequences used in
CC the exemplification of the present invention.

Q Sequence 333 AA;

Query Match 99.7%; Score 1725; DB 21; Length 333;
Best Local Similarity 99.7%; Pred. No. 2.6e-172;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNTVMQGFNRSEKPRDTRIVQVLPALYTVVFLTGILLNTLALWVFIHPSSSTFIY 60
DB 1 MNTVMQGFNRSEKPRDTRIVQVLPALYTVVFLTGILLNTLALWVFIHPSSSTFIY 60
OY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCRSSVIFYETMYGIVLGLIAFDR 120
DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCRSSVIFYETMYGIVLGLIAFDR 120
OY 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSYKRCASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSYKRCASLKGPL 180
OY 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKVVDSYRKSCKDRKNNKLEGVFVV 240
DB 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKVVDSYRKSCKDRKNNKLEGVFVV 240
OY 241 AVFVCFAPFHFARVPYTHSQTNNKTCRQLNQLFIKETTFLAATNIGMDPLIYIFLC 300
DB 241 AVFVCFAPFHFARVPYTHSQTNNKTCRQLNQLFIKETTFLAATNIGMDPLIYIFLC 300
OY 301 KKFTKLPQMGGRKTTASSQENHSSQTDNITLG 333
DB 301 KKFTKLPQMGGRKTTASSQENHSSQTDNITLG 333

RESULT 7
AAU10588 standard; Protein; 333 AA.
XX
AC AAU10588;

DT 25-FEB-2002 (first entry)

DE Human HNEA81 polypeptide sequence.

KW Human; HNEA81; G-protein coupled receptor; bacterial infection; cancer;
KW fungal infection; protozoal infection; viral infection; HIV-1; HIV-2;
KW human immunodeficiency virus; pain; anorexia; bulimia; asthma; allergy;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcer; benign prostatic hypertrophy; neurological disorder; anxiety;
KW schizophrenia; manic depression; dementia; delirium; psychotic disorder;
KW severe mental retardation; dyskinesia; Huntington's disease;
KW Gilles de la Tourette's syndrome.

OS Homo sapiens.

XX US2001021509-A1.
PN

XX 13-SEP-2001.
PD
XX
PF 24-JAN-2001; 2001US-0769159.
XX
PR 28-DEC-1998; 98US-0221456.
PR 26-APR-2000; 2000US-0558740.
PR 23-OCT-1997; 97US-0956975.

XX (SATH/) SATHE G M.
PA (HALS/) HALSEY W S.
PA (CHAM/) CHAMBERS J.
PA (MUIR/) MUIR A.
PA (SZEK/) SZEKERES P.

PI Sathe GM, Halsey WS, Chambers J, Muir A, Szekeres P;
XX
XX WPI: 2001-595775/67.
DR N-PSDB; AAS16912.

PT New HNEA81 polypeptides and polynucleotides, useful for treating
PT infections, e.g. bacterial, fungal, protozoal and viral infections,
PT pain, cancers, psychotic and neurological disorders and severe mental
PT retardation

XX Claim 2; Page 6; 16pp; English.

CC The invention relates to the human HNEA81 polypeptide and its associated
CC DNA sequence. These sequences are related to the G-protein coupled
CC receptor family. The HNEA81 polypeptides are useful for treating
CC bacterial, fungal, protozoal and viral infections, particularly
CC infections caused by human immunodeficiency virus (HIV)-1 or HIV-2, pain,
CC cancers, anorexia, bulimia, asthma, Parkinson's disease, acute heart
CC failure, hypotension, hypertension, urinary retention, osteoporosis,
CC angina pectoris, myocardial infarction, ulcer, allergies, benign
CC prostatic hypertrophy, psychotic and neurological disorders (such as
CC anxiety, schizophrenia, manic depression and dementia), delirium, severe
CC mental retardation and dyskinesias (such as Huntington's disease and
CC Gilles de la Tourette's syndrome). The polypeptides may also be used as
CC research agents and material for the discovery of treatments and
CC diagnostics for human and animal diseases, for screening compounds that
CC bind to and activate the HNEA81 polypeptides and for assessing the
CC binding of small molecule substrates and ligands in cells, cell-free
CC preparations, chemical libraries and natural product mixtures. This
CC sequence represents the human HNEA81 polypeptide.

XX Sequence 333 AA;

Query Match 99.7%; Score 1725; DB 22; Length 333;
Best Local Similarity 99.7%; Pred. No. 2.6e-172;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MNTVMQGFNRSEKPRDTRIVQVLPALYTVVFLTGILLNTLALWVFIHPSSSTFIY 60
DB 1 MNTVMQGFNRSEKPRDTRIVQVLPALYTVVFLTGILLNTLALWVFIHPSSSTFIY 60
OY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCRSSVIFYETMYGIVLGLIAFDR 120
DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCRSSVIFYETMYGIVLGLIAFDR 120
OY 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSYKRCASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSYKRCASLKGPL 180
OY 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKVVDSYRKSCKDRKNNKLEGVFVV 240
DB 181 GLKWHQMVNNICQFIWTVFILMLVEYVVIKVVDSYRKSCKDRKNNKLEGVFVV 240
OY 241 AVFVCFAPFHFARVPYTHSQTNNKTCRQLNQLFIKETTFLAATNIGMDPLIYIFLC 300
DB 241 AVFVCFAPFHFARVPYTHSQTNNKTCRQLNQLFIKETTFLAATNIGMDPLIYIFLC 300
OY 301 KKFTKLPQMGGRKTTASSQENHSSQTDNITLG 333

DB 301 KKFTEKLPQMGGRKTTASSQENHSSQTDNITLG 333

RESULT 8
AAB31580

ID AAB31580 standard; Protein; 333 AA.

XX AAB31580;

DT 20-APR-2001 (first entry)

DE Amino acid sequence of a human HNEAA81 polypeptide.

XX Human; HNEAA81; infection; pain; cancer; anorexia; bulimia; asthma;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcer; asthma; allergy; benign prostatic hypertrophy; psychotic disorder;
KW neurological disorder; anxiety; schizophrenia; manic depression;
KW delirium; dementia; severe mental retardation; dyskinesia;
KW Huntington's disease; Gilles de la Tourette's syndrome.

XX Homo sapiens.

XX US6162899-A.

PD 19-DEC-2000.

XX 28-DEC-1999; 99US-0221456.

XX 23-OCT-1997; 97US-0956975.

XX (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.

XX Halsey WS, Chambers J, Sathe GM, Szekeres P, Muir A;
DR WPI; 2001-090409/10.
N-PSDB; AAF24909.

XX Novel human HNEAA81 receptor polypeptides useful for treating microbial
PT infections, cancer, asthma, Parkinson's disease, hypertension, urinary
PT retention, osteoporosis, angina pectoris, myocardial infarction
XX Claim 1; Column 11-12; 16pp; English.

XX The present sequence represents a human HNEAA81 polypeptide. The
CC polypeptide is useful for the treatment of infections, such as bacterial,
fungal, protozoan or viral, particularly infections caused by HIV-1 or
HIV-2, pain, cancers, anorexia, bulimia, asthma, Parkinson's disease,
acute heart failure, hypotension, hypertension, urinary retention,
osteoporosis, angina pectoris, myocardial infarction, ulcers, asthma,
allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders, including anxiety, schizophrenia, manic depression,
CC delirium, dementia, severe mental retardation and dyskinesias, such as
CC Huntington's disease or Gilles de la Tourette's syndrome.

XX Sequence 333 AA;

Query Match 99.7%; Score 1725; DB 22, Length 333;
Best Local Similarity 99.7%; Pred. No. 2.6e-172;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNTVMQGFNRSECRPRDRIQVLVFPALYTVFLTGILNTYALMVFVHIPSSSTFIYY 60
DB 1 MNTVMQGFNRSECRPRDRIQVLVFPALYTVFLTGILNTYALMVFVHIPSSSTFIYY 60

QY 61 LKNTLVADLIMTLMFPKTIISDSLAPWQLRAFCRSSVIFETMYVGIVLLGLIAFDR 120
DB 61 LKNTLVADLIMTLMFPKTIISDSLAPWQLRAFCRSSVIFETMYVGIVLLGLIAFDR 120

QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNTILSNKEATPSSVKKCASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNTILSNKEATPSSVKKCASLKGPL 180

DB 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNTILSNKEATPSSVKKCASLKGPL 180

QY 181 GLKWHQVNNICQFIETVFIIMLVFVYVIAKKVYDSYRKS SKDRNNKKEGKVFVVV 240
DB 181 GLKWHQVNNICQFIETVFIIMLVFVYVIAKKVYDSYRKS SKDRNNKKEGKVFVVV 240

QY 241 AVEFVCFAPFHFARVPYTHSQTNNKTCRQNLFIAKETTLFLAATNICMDPLIYIFLC 300
DB 241 AVEFVCFAPFHFARVPYTHSQTNNKTCRQNLFIAKETTLFLAATNICMDPLIYIFLC 300

QY 301 KKFTEKLPQMGGRKTTASSQENHSSQTDNITLG 333
DB 301 KKFTEKLPQMGGRKTTASSQENHSSQTDNITLG 333

RESULT 9
AAE02494

ID AAE02494 standard; Protein; 333 AA.

XX AAE02494;

DT 10-AUG-2001 (first entry)

DE Human CON203 G protein-coupled receptor protein.

XX Human; G protein-coupled receptor; GPCR; CON203 protein; schizophrenia;
KW neuroleptic; nootropic; neuroprotective; bipolar disease; psychotropic;
KW neurological disorder; psychiatric disease; neurosis; anxiety; neuritis;
KW attention deficit hyperactivity disorder; neuroasthenia; senile dementia;
KW affective disorder; neuropathy; Alzheimer's disease; Parkinson's disease;
KW depression; migraine; genetic screening; chromosome 3.

XX Homo sapiens.

XX Location/Qualifiers
FH 29..53
FT /label= Transmembrane_domain_(1TM)
FT 54..62
FT /label= Intracellular_domain
FT /note= "First IC loop"
FT 63..82
FT /label= Transmembrane_domain_(2TM)
FT 83..96
FT /label= Extracellular_domain
FT /note= "First EC loop"
FT 97..118
FT /label= Transmembrane_domain_(3TM)
FT 119..135
FT /label= Intracellular_domain
FT /note= "Second IC loop"
FT 136..160
FT /label= Transmembrane_domain_(4TM)
FT 161..188
FT /label= Extracellular_domain
FT /note= "Second EC loop"
FT 189..211
FT /label= Transmembrane_domain_(5TM)
FT 212..231
FT /label= Intracellular_domain
FT /note= "Third IC loop"
FT 232..252
FT /label= Transmembrane_domain_(6TM)
FT 253..280
FT /label= Extracellular_domain
FT /note= "Third EC loop"
FT 281..300
FT /label= Transmembrane_domain_(7TM)

WO200131014-A2.

03-MAY-2001.

27-OCT-2000; 2000WO-US29601.


```
AC AAB62472;
XX
DT 09-JUL-2001 (first entry)
XX
DE Rat 7-transmembrane receptor, rHNEAA81.
XX
KW 7-transmembrane receptor; rHNEAA81; G-protein coupled receptor; GPCR;
KW antiHIV; cytostatic; antidiabetic; anorectic; antiaschmatic; osteopathic;
KW antiparkinsonian; hypotensive; antianal; cerebral protective; antitumor;
KW antimigraine; antiallergic; neuroprotective; antidepressant; rat;
KW antimicrobial; gene therapy.
XX
OS Rattus sp.
XX
PN WO200129089-A1.
XX
PD 26-APR-2001.
XX
PF 19-OCT-2000; 2000WO-US28906.
XX
PR 19-OCT-1999; 99US-0160438.
PR 18-OCT-2000; 2000US-0691271.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Trlnh HN;
XX
DR WPI; 2001-308478/32.
DR N-PSDB; AAF57695.
XX
PT New rat 7-transmembrane receptor (G-protein coupled receptor (GPCR)),
PT rHNEAA81 polypeptide useful for treating infections, pain,
PT cancer, diabetes, obesity, anorexia, bulimia, autism and Parkinson's
PT disease
XX
PS Claim 2; Page 35; 39pp; English.
XX
CC This represents a rat 7-transmembrane receptor, rHNEAA81
CC polypeptide belonging to the family of G-protein coupled receptor (GPCR).
CC The rHNEAA81 is useful for treating bacterial, fungal, protozoan and
CC viral infections, particularly infections caused by HIV-1 or HIV-2, pain,
CC cancer, diabetes, obesity, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, stroke,
CC ulcers, asthma, allergies, benign prostatic hypertrophy, migraine,
CC vomiting, psychotic and neurological disorders including anxiety,
CC schizophrenia, manic depression, depression, delirium, dementia and
CC severe mental retardation, and dyskinesias, such as Huntington's disease
CC or Gilles de la Tourette's syndrome.
XX
SQ Sequence 336 AA;
XX
Query Match 81.0%; Score 1402.5; DB 22; Length 336;
Best Local Similarity 80.2%; Pred. No. 1.6e-138;
Matches 267; Conservative 29; Mismatches 34; Indels 3; Gaps 3;
OY 1 MNTTVMOGFNRSERCPDRTRIVOLVFPALYTVVFLTGILLNTLALMWVFIHPSSTFIY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 5 VNTTGMGFNKSERCPDRTRMTOLEPVLVTVVFTGVLNTLALMWFIHPSNSTFIY 64
OY 61 LKNTLVADLIMTLMPFKILSDSHLAPWQLRAFCRSSVFYETMYVGIVLGLIAFDR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 65 LKNTLVADLIMTLMPFKILSDSLAPWQLRGFCVTFSSVFYETMYVGIMLGLIAFDR 124
OY 121 FLKTIPLRNIFLKKPVFAKTVSFIWFLEFISLPNMISNKEATPSSVKKCASKLGPL 180
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 125 FLKTIVPFRKTFVKTAFAKIVSISIMLMLFSLPNMIL-NKEATASTVKKCASKLSP 183
OY 181 GLKWHQVNNICQIFWTVFILMVEVVIKAVYDSYRKSRSKDRKNNKLEGVFVVV 240
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 184 GLLMHQVYSHTCQIFWTVFILMVEVVIKAVYDSYRKSRSKDRKNNKLEGVFIVM 242
```

```
OY 241 AVFVCFAPFPHARVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIFLC 300
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 243 AVFVCFAPFPHARVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIILC 302
OY 301 KKFTKLPFCMOGR-KTASSQENHSSQTDNITL 332
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 303 KKFTKVPFCMRWRTKTAASSDEHHSSQTDNITL 335
RESULT 12
AAB73484
ID AAB73484 standard; Protein; 337 AA.
XX
AC AAB73484;
XX
DT 09-JUL-2001 (first entry)
XX
DE Mouse G protein-coupled receptor mHNEAA81.
XX
KW Mouse; mHNEAA81; G protein-coupled receptor; GPCR; 7TM receptor;
KW 7 transmembrane domain receptor; infection; viral; bacterial; fungal;
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;
KW bulimia; osteoporosis; asthma; allergy; urinary retention;
KW acute heart failure; hypotension; hypertension; angina pectoris;
KW myocardial infarction; stroke; ulcer; migraine; vomiting;
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;
KW manic depression; bipolar disorder; depression; delirium; dementia;
KW severe mental retardation; dyskinesia; Parkinson's disease;
KW Huntington's disease; Gilles de la Tourette's syndrome;
KW transgenic animal; drug screening; signal transduction;
KW agonist; antagonist; human KIAA001 homologue.
XX
OS Mus musculus.
XX
PN WO200127153-A1.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US28304.
XX
PR 13-OCT-1999; 99US-0159217.
PR 12-OCT-2000; 2000US-0689582.
XX
PA (SMIK ) SMITHKLINE BEECHAM CORP.
PA (SMIK ) SMITHKLINE BEECHAM PLC.
XX
PI Taylor AH, Ames RS, Sarau HM, Foley JT;
XX
DR WPI; 2001-290711/30.
DR N-PSDB; AAF84498.
XX
PT Mus musculus mHNEAA81 polypeptide for production of agonists and
PT antagonists for treatment of diseases e.g. infections, cancers,
PT psychotic and neurologic disorders
XX
PS Claim 2; Page 37; 45pp; English.
XX
CC This sequence represents the mouse mHNEAA81 protein. The mouse mHNEAA81
CC protein is a member of the G protein-coupled receptor (GPCR) superfamily,
CC and like all GPCRs, mouse mHNEAA81 has 7 putative transmembrane domains
CC and is involved in signal transduction. In particular, mouse mHNEAA81
CC has homology to human KIAA001. The invention also relates to expression
CC vectors and host cells comprising mHNEAA81 DNA, to recombinant
CC expression of mHNEAA81, to drug screening methods that use mouse
CC mHNEAA81 and to mHNEAA81 agonists and antagonists. Mouse mHNEAA81
CC nucleic acid sequences may be used to isolate cDNA and/or genomic clones
CC encoding mHNEAA81 homologues or orthologues, particularly from other
CC species, and may also be used in chromosome localisation studies. Mouse
CC mHNEAA81 nucleotides may be used to generate transgenic animals,
CC including knockout animals, which may provide an insight into treating a
CC variety of human disorders. Such disorders include bacterial, fungal,
CC protozoal and viral infections, particularly HIV-1 or HIV-2 infections,
CC pain; cancers; benign prostatic hypertrophy; diabetes; obesity; anorexia;
```

bulimia; osteoporosis; asthma; allergies; urinary retention; acute heart failure; hypotension; hypertension; angina pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting; psychotic and neurological disorders such as anxiety, schizophrenia, manic depression, depression, delirium, dementia, and severe mental retardation, and dyskinesias, such as Parkinson's disease, Huntington's disease or Gilles de la Tourette's syndrome. MHNPA81 proteins and nucleotides may also be used in screening compounds for their ability to modulate MHNPA81 activity or expression.

SQ Sequence 337 AA;

Query Match	79.38;	Score 1372;	DB 22;	Length 337;
Best Local Similarity	77.88;	Pred. No. 2.6e-135;		
Matches 260;	Conservative 34;	Mismatches 36;	Indels 4;	Gaps 3;

QY	1	MNTVMÖGFNRSERCPRDTRIÖVLPEPALYTVFLLTGILLNTLALMVEFHIPSSSTFEIY	60
Db	5	INTGMÖGFNKSESRCPDRTRMÖQLPEVPYLVTVFLAGILLNTVALMVEFHIPSNSTFEIY	64
LY	61	LKNTLVADLIMTLMLPFKILSDSHLAPWÖLRAFCVCRSSVIFYETMYVGIYLLGLIAFDR	120
Db	65	LKNTLVADLIMALMLPFKILSDSHLAPWÖLGRFVCTLSSVIFYETMYVGIMMGLIAFDR	124
QY	121	FLKIIRPLRNIFLKKPVPFAKTVSIFIMFLEFISLPMILSNKEATPSSYKCKASLKGPL	180
Db	125	FLKIIMPERKTEFVKKTAFAKTVSISVWSLMEFISLPMIL-NKEATPSSYKCKASLKSPL	183
QY	181	GLKWHÖMVNNICÖFIEWTVFILMLVEYVYIAKKVYDSYRKSkskDRKNNKKLEGVVVV	240
Db	184	GLMWHÖVVSHTCÖFIEMAVFILMLLEYAVITKKVYNSYRKFRSKDSR-HKRLEVKVFIVM	242
QY	241	AVFEVFCFAPFHEARVPYTHSÖTNNKTDCLÖNÖLFIAKETTLFLAATNICMDPLIYIFLC	300
Db	243	AVFEVFCFAPLHEVRIPYTHSÖTNNKTDCLRNÖLFIAKEATTLFLATNICMDPLIYIILC	302
QY	301	KKFTEKLPCMÖGRK--TTASSÖENHSSÖTDNITL	332
Db	303	KKFTÖKVPCVRRWGKARTAGSSÖDHSSÖTDNITL	336

RESULT	13
ID	AAW04246 standard; Protein; 293 AA.
XX	
AC	AAW04246;
XX	
DT	13-DEC-1996 (first entry)
XX	
DE	Human G-protein coupled receptor GPR3.
XX	
KM	G-protein coupled receptor; GPR3; signal transduction; agonist;
KW	antagonist; cell proliferation; cancer; tumour; asthma; allergy;
XX	diagnosis.
XX	
OS	Homo sapiens.
XX	
PN	WO9630406-A1.
XX	
PD	03-OCT-1996.
XX	
PF	30-MAR-1995; 95WO-US04079.
XX	
PR	30-MAR-1995; 95WO-US04079.
XX	
PA	(HUMA-) HUMAN GENOME SCI INC.
XX	
PI	Bult CJ, Cao L, Gentz R, Li Y, Nii J, Rosen CA;
PI	Sutton GG;
XX	
DR	WPI; 1996-455278/45.
DR	N-PSDB; AAT33904.
XX	

PT Nucleic acid encoding human G-protein coupled receptor - for
PT diagnosing diseases, and identifying (ant)agonists for asthma and
PT allergy treatment

PS Claim 1; Page 55-56; 87pp; English.

CC Novel human G-protein coupled receptor GPR3 (AAW04246) was identified
CC as the product of a cDNA clone (AAT33904) isolated from human
CC neutrophils. The protein is also expressed in the human liver,
CC kidney and pancreas. It shows 39% identity with a known human
CC G-protein coupled receptor. Potential ligands include platelet
CC activating factor, thrombin, c5a and bradykinin. Recombinant GPR3,
CC GPR1, GPR2 and GPR4 (see also AAW04244-45 and AAW04247) can be
CC expressed in e.g. E. coli, COS or insect cell hosts for use in
CC identifying (ant)agonist cpds. Agonists may be used to treat asthma,
CC Parkinson's disease, hypotension, osteoporosis etc., and antagonists
CC to treat ulcers, asthma, allergies, etc.

SQ Sequence 293 AA;

Query Match	63.5%	Score 1098.5;	DB 17;	Length 293;
Best Local Similarity	76.8%;	Pred. No. 9.8e-107;		
Matches 225;	Conservative 14;	Mismatches 43;	Indels 11;	Gaps 4;

```
QY      1 MNTTVMOGFNSESRCPDRTRIVOLVFPALYTVEFLTGILLNTLALMVFVHIPSSSTFIIX 60
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MNTTVMOGFNRSKRCPKDRIVOLVFPALYTVEFLTGILLNTLALMVFVHIPSSSTFIIX 60

QY      61 LKNTLVADILMTLMLEPKILSDSHLAPWQLRAFCRSSVIFETMYVGIVLLGLIADFDR 120
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 LKNTLVADILMTLMLEPKILSDSHLAPWQLRAFCRSSVIFETMYVGIVLLGLIADFDR 120

QY      121 FLKIIRPLRNITFLKKPVFAKTVSIFIMEFLEFISLPNMILSNKEATPSSVKKCASLKGPL 180
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      121 FLKIIRPLRNITFLKKPVWGKTVSIFIMEFEFISLPNMIILSNKEATPSSVKKCASLKGPL 180

QY      181 GLKWHOMVNINICOFIEWTFEITMLVEFYVIIAKKVYDSYRKSXSKDRKNKKLEGKYF--- 237
        |||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      181 GLKWHOMVNINICOFIEWTFEITMLVEFYVIIAKKYMILIESPRVTEKTKSMWAKAYILSW 240

QY      238 ---VVVAFFVCFAPFHFARVPYTHSOTNNKTDCLRONOLFIAKETTLFLAAT 287
        :||::||:|:||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      241 LSSLCVLLHFIIS-PEFHILTVPKPTIRLT--VDCKI-NCLLIKKOOLSFWOOLT 288
```

RESULT 14	
XX AAB15412	
ID AAB15412	standard; protein; 293 AA.
XX AC AAB15412;	
XX DT 17-JAN-2001	(first entry)
XX DE Human G-protein coupled receptor GRP-3.	
XX KM Human; G-protein coupled receptor; GRP-3; 7-transmembrane receptor; ds	
KW neutrophil; hybridization probe; diagnostic; tumour; cancer; mutation.	
XX OS Homo sapiens.	
XX PN US6090575-A.	
XX PD 18-JUL-2000.	
XX PF 06-JUN-1995;	95US-0467947.
XX PR 30-MAR-1995;	95WO-US04079.
XX PA (HUMA-) HUMAN GENOME SCI INC.	
XX PI LI Y, Gentz R, Bult CJ, Sutton GG, Rosen CA, Cao L, Ni J;	
XX DR WPI; 2000-514035/46.	

DR N-PSDB; AAA70770.
XX
PT Polynucleotide encoding a G-protein coupled receptor polypeptide useful
PT as a hybridization probe for screening a cDNA library and the
PT polypeptide encoded useful for screening antagonist and agonist
XX
PS Disclosure: Fig 3A-C; 52pp; English.
XX
CC This sequence represents a novel human G-protein coupled receptor 3
CC (GRP-3), which is a human 7-transmembrane receptor. The coding sequence
CC was isolated from a human neutrophil cDNA library and deposited as ATCC
CC 75979. The coding sequence was subcloned into the vector pQE3 for
CC expression in bacterial cells and pCDNA1/Amp for expression in COS cells.
CC The DNA is useful as a hybridization probe for a cDNA library to isolate
CC the full length cDNA and to isolate other cDNAs which have a high
CC sequence similarity to the gene or similar biological activity. It is
CC also useful for diagnosing by detecting diseases such as tumours and
CC cancers or susceptibility to diseases related to presence of mutations
CC in the DNA.
XX
SQ Sequence 293 AA;

Query Match 63.5%; Score 1098.5; DB 21; Length 293;
Best Local Similarity 76.8%; Pred. No. 9.8e-107;
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

QY 1 MNTTMOGFNRSEKPRDTRIVQLVLPALYTVFLLGILLNTIALMVFVHIPSSSTFIIT 60
DB 1 MNTTMOGFNRSKRCPDTRIVQLVLPALYTVFLLGILLNTIALMVFVHIPSSSTFIIT 60

QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFETMYVGIVLLGLIAFDR 120
DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFETMYVGIVLLGLIAFDR 120

QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVGKTVSIFWFFLFISLPMILSNKEATPSSVKKASLKGPL 180

QY 181 GLKWHQMVNNICQFIWTVFILLMVFYVIAKKYDYSYRKSCKDRKNNKLEKGF--- 237
DB 181 GLKWHQMVNNICQFIWTVFILLMVFYVIAKKYMTLIESPKVTEKTKSWKAKYLLSW 240

QY 238 ---VVAVFVFCFAPFHFARVPYTHSQTNNKTDCLONQLFIKETTFLAAT 287
DB 241 LSSLCLVLLHFIS-PEFHILTVKPTIRLT---VDCKI-NCLLLKKQLSFWOQLT 288

RESULT 15
Y67355
AAV67355 standard; Protein; 293 AA.
AX AAV67355;
AC AAV67355;
XX
DT 25-APR-2000 (first entry)
XX
DE Human G-protein coupled receptor GPR3 amino acid sequence.
XX
KW G-protein coupled receptor; GPR3; human; ATCC #75979; tumour; cancer;
KW diagnose.
XX
OS Homo sapiens.
XX
PN US5998164-A.
XX
PD 07-DEC-1999.
XX
PF 06-JUN-1995; 95US-0467948.
XX
PR 30-MAR-1995; 95WO-US04079.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI LI Y, Gentz R, Bult CJ, Sutton GG, Rosen CA, Cao L, Ni J;

XX
DR WPI; 2000-125626/11.
DR N-PSDB; AAZ67356.
XX
PT Genes useful in assays for diagnosing tumours and cancers
XX
PS Example 3; Fig 3; 51pp; English.
XX
CC This sequence represents a human G-protein coupled receptor GPR3 amino
CC acid sequence given ATCC deposit number 75979. The nucleotide sequence
CC encoding GPR3 was isolated from human liver, kidney and pancreas. The
CC invention relates to G-protein coupled receptor GPR2 (see AAZ60117)
CC which has ATCC number 75976. The GPR2 polypeptide is used as part of a
CC diagnostic assay for detecting diseases or susceptibility to diseases
CC related to the presence of mutations in the GPR2 polypeptide. Examples
CC of the diseases include tumours and cancers related to cell
CC transformations. Nucleic acid sequences which specifically hybridise to
CC the nucleic acid sequences encoding GPR2 can be used as diagnostic
CC probes.
XX
SQ Sequence 293 AA;

Query Match 63.5%; Score 1098.5; DB 21; Length 293;
Best Local Similarity 76.8%; Pred. No. 9.8e-107;
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

QY 1 MNTTMOGFNRSEKPRDTRIVQLVLPALYTVFLLGILLNTIALMVFVHIPSSSTFIIT 60
DB 1 MNTTMOGFNRSKRCPDTRIVQLVLPALYTVFLLGILLNTIALMVFVHIPSSSTFIIT 60

QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFETMYVGIVLLGLIAFDR 120
DB 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFETMYVGIVLLGLIAFDR 120

QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVGKTVSIFWFFLFISLPMILSNKEATPSSVKKASLKGPL 180

QY 181 GLKWHQMVNNICQFIWTVFILLMVFYVIAKKYDYSYRKSCKDRKNNKLEKGF--- 237
DB 181 GLKWHQMVNNICQFIWTVFILLMVFYVIAKKYMILIESPKVTEKTKSWKAKYLLSW 240

QY 238 ---VVAVFVFCFAPFHFARVPYTHSQTNNKTDCLONQLFIKETTFLAAT 287
DB 241 LSSLCLVLLHFIS-PEFHILTVKPTIRLT---VDCKI-NCLLLKKQLSFWOQLT 288

Search completed: October 11, 2002, 14:48:41
Job time : 35 secs

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On protein - protein search, using sw model

Run on: October 11, 2002, 14:47:00 ; Search time 30 Seconds

(without alignments)
1920.244 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731

Sequence: 1 MNTVMQGFNRSEKPRDTR.....KTPASSQENHSSQTDNITLG 333

Scoring table: BLOSUM62

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : SPTREMBL 19:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriophage:*
 - 17: sp_archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1731	100.0	333	4	Q9BPV8
2	1366	78.9	337	11	Q9D8I2
3	1128	65.2	228	6	Q9BE53
4	928	53.6	176	4	Q9BY61
5	833	48.1	342	6	Q9SKC3
6	830	47.9	342	6	Q9BGT8
7	829	47.9	342	4	Q9H244
8	813	47.0	347	11	Q9CPV9
9	807	46.6	343	11	Q9EPX4
10	767.5	44.3	338	11	Q9ESG6
11	692.5	40.0	358	4	Q9BY21
12	692.5	40.0	358	4	Q9BJZ8
13	681.5	39.4	359	11	Q99MT7
14	541.5	31.3	269	4	Q9BXC2
15	363.5	21.0	367	4	Q9UE21
16	339.5	19.6	337	4	Q9Y271

17	337.5	19.5	340	6	Q95N02	Q95N02 sus scrofa
18	331	19.1	342	6	Q9GK76	Q9GK76 capra hircu
19	330.5	19.1	298	4	Q9UD26	Q9UD26 homo sapien
20	326	18.8	342	6	Q9XSD4	Q9XSD4 sus scrofa
21	326	18.8	342	6	Q9TTY5	Q9TTY5 bos taurus
22	320.5	18.5	339	11	Q924T8	Q924T8 rattus norv
23	318.5	18.4	339	11	Q9JJ71	Q9JJ71 mus musculu
24	318.5	18.4	352	11	Q99JA4	Q99JA4 mus musculu
25	315.5	18.2	352	11	Q9JK47	Q9JK47 mus musculu
26	310.5	17.9	296	6	Q9TTY6	Q9TTY6 canis famli
27	310.5	17.9	361	11	Q9JJS7	Q9JJS7 mus musculu
28	304.5	17.6	359	6	Q9N0U1	Q9N0U1 ovis aries
29	304	17.6	359	11	Q9EPP3	Q9EPP3 cavia porce
30	303.5	17.5	361	11	Q958I1	Q958I1 rattus norv
31	302	17.4	377	13	Q98U14	Q98U14 brachydantio
32	301.5	17.4	359	6	Q9GLN9	Q9GLN9 pan troglod
33	300	17.3	374	13	Q95785	Q95785 brachydantio
34	300	17.3	374	13	Q9JLZ0	Q9JLZ0 melalegris g
35	298	17.2	380	13	Q9DGO6	Q9DGO6 carassius a
36	295.5	17.1	360	6	Q9BG77	Q9BG77 pan troglod
37	293.5	17.0	361	13	Q90X57	Q90X57 xenopus lae
38	293	16.9	400	6	Q95M54	Q95M54 macaca fasc
39	292	16.9	454	4	Q9H573	Q9H573 homo sapien
40	290	16.8	362	11	Q9JLZ0	Q9JLZ0 rattus norv
41	290	16.8	362	11	Q9JLW0	Q9JLW0 mus musculu
42	289.5	16.7	383	13	Q42324	Q42324 catostomus
43	287	16.6	359	11	Q9EOR9	Q9EOR9 meriones un
44	287	16.6	400	6	Q9MYW9	Q9MYW9 macaca mula
45	286	16.5	393	11	Q9R1M0	Q9R1M0 mus musculu

ALIGNMENTS

RESULT 1	ID	Q9BPV8	PRELIMINARY;	PRT;	333 AA.
AC	Q9BPV8;				
DT	01-JUN-2001	(TREMBLREL. 17, Created)			
DT	01-JUN-2001	(TREMBLREL. 17, Last sequence update)			
DT	01-DEC-2001	(TREMBLREL. 19, Last annotation update)			
DE	PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR GPR86) (G PROTEIN-COUPLED RECEPTOR)				
DE	GPR86)				
GN	FKSG77 OR GPR86 OR GPR94.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID-9606;				
RN	[1]	SEQUENCE FROM N.A.			
RP	TISSUE=HEART;				
RA	Wang Y., Gong L.;				
RT	"Molecular cloning of FKSG77, a novel gene encoding a putative G-				
RT	protein-coupled receptor."				
RL	Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.				
RN	[2]	SEQUENCE FROM N.A.			
RP	MEDLINE-21172992; PubMed-11273702;				
RX	Wittenberger T., Schaller H.C., Hellebrand S.;				
RT	"An expressed sequence tag (est) data mining strategy succeeding in				
RT	the discovery of new g-protein coupled receptors."				
RL	J. Mol. Biol. 307:799-813(2001).				
RN	[3]	SEQUENCE FROM N.A.			
RP	MEDLINE-21458557; PubMed-11574155;				
RX	Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantli W.B., Arkhitko O.,				
RA	Lewis T., Evans J.F., George S.R., O'Dowd B.F.;				
RT	"Discovery and mapping of ten novel G protein-coupled receptor				
RT	genes."				
RL	Gene 275:83-91(2001).				
RN	[4]	SEQUENCE FROM N.A.			

RX PubMed-11546776;
RA Communi D., Gonzalez N.S., Dethaux M., Brezillon S., Iannoy V.,
RA Parentlet M., Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to G1.";
RJ J. Biol. Chem., 276:41479-41485(2001).
DR EMBL; AF345565; AAK29068.1; -
DR EMBL; AF295368; AAK01864.1; -
DR EMBL; AF41113; AAL26484.1; -
DR EMBL; AF406692; AAL01038.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR Receptor.
SQ SEQUENCE 333 AA; 38440 MW; F234AB50016DF34 CRC64;

Query Match 100.0%; Score 1731; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 7.8e-147;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTVMQGFNRSECRPDRTRIVQLVLPALYTVVFLTGILNTLALMVFVHIPSSSTFIIT 60
DB 1 MNTVMQGFNRSECRPDRTRIVQLVLPALYTVVFLTGILNTLALMVFVHIPSSSTFIIT 60
QY 61 LKNTLVADLIMTLMPFKILSDSHLAPWQLRAVFCRSSVIFETMYVGIVLGLIAFDR 120
DB 61 LKNTLVADLIMTLMPFKILSDSHLAPWQLRAVFCRSSVIFETMYVGIVLGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMLSNKEATPSSVKKCASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMLSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKRVDSYRSKSKDRKNNKLEGVFVVV 240
DB 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKRVDSYRSKSKDRKNNKLEGVFVVV 240
QY 241 AVEFVCFAPHFARVPYTHSQNNKTDCLQNLQFLIAKETTLFLAATNICMDPLIYIFLC 300
DB 241 AVEFVCFAPHFARVPYTHSQNNKTDCLQNLQFLIAKETTLFLAATNICMDPLIYIFLC 300
QY 301 KKFTKLPKMGKRTTASSQENHSSQTDNITLG 333
DB 301 KKFTKLPKMGKRTTASSQENHSSQTDNITLG 333

Q9DB12 PRELIMINARY; PRT; 337 AA.
Q9DB12
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE 2010001L06RIK PROTEIN.
GN GPR05 OR 2010001L06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=SMALL INTESTINE;
RX MEDLINE-21085680; PubMed-11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008013; BAB25409.1; -
DR MGI; 1921441; GPR86.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
DR SEQUENCE 337 AA; 38693 MW; 2C1A76FBF893D5EA CRC64;

Query Match 78.9%; Score 1366; DB 11; Length 337;
Best Local Similarity 77.5%; Pred. No. 3.1e-114;
Matches 259; Conservative 34; Mismatches 37; Indels 4; Gaps 3;

QY 1 MNTVMQGFNRSECRPDRTRIVQLVLPALYTVVFLTGILNTLALMVFVHIPSSSTFIIT 60
DB 5 INTGMQGNKSECRPDRTRIVQLVLPALYTVVFLTGILNTLALMVFVHIPSSSTFIIT 64
QY 61 LKNTLVADLIMTLMPFKILSDSHLAPWQLRAVFCRSSVIFETMYVGIVLGLIAFDR 120
DB 65 LKNTLVADLIMTLMPFKILSDSHLAPWQLRGVCTLSVVFETMYVGIMLGLIAFDR 124
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMLSNKEATPSSVKKCASLKGPL 180
DB 125 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMLSNKEATPSSVKKCASLKGPL 183
QY 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKRVDSYRSKSKDRKNNKLEGVFVVV 240
DB 184 GLWHDVYVSHTCQILFVAVFVAVITKVVNSYRFRSKDSR-HKRLVAVFV 242
QY 241 AVEFVCFAPHFARVPYTHSQNNKTDCLQNLQFLIAKETTLFLAATNICMDPLIYIFLC 300
DB 243 AVEFVCFAPHFARVPYTHSQNNKTDCLQNLQFLIAKETTLFLAATNICMDPLIYIFLC 302
QY 301 KKFTKLPKMGKRTTASSQENHSSQTDNITLG 332
DB 303 KKFTKLPKMGKRTTASSQENHSSQTDNITLG 336

RESULT 3
Q9BE53 PRELIMINARY; PRT; 228 AA.
Q9BE53
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID-9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL CORTEX;
RA Otsuda N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056816; BAB39342.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.

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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:48:00 ; Search time 19 Seconds
(without alignments)
428.091 Million cell updates/sec

Title: US-09-924-125-2
Perfect score: 1731
Sequence: 1 MNTVMQGFNRSEKPRDTR.....KTASSQENISSQTDNITLG 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1725	99.7	333	4	US-09-221-456-2 Sequence 2, Appl1
2	1725	99.7	333	4	US-09-558-740-2 Sequence 2, Appl1
3	1697	98.0	333	2	US-08-812-871-1 Sequence 1, Appl1
4	1098.5	63.5	293	2	US-08-467-948A-6 Sequence 6, Appl1
5	1098.5	63.5	293	3	US-08-467-947A-6 Sequence 6, Appl1
6	829	47.9	342	3	US-08-852-824-2 Sequence 2, Appl1
7	777	44.9	325	2	US-08-467-948A-29 Sequence 29, Appl1
8	777	44.9	325	3	US-08-467-947A-29 Sequence 29, Appl1
9	777	44.9	338	3	US-08-988-876-8 Sequence 8, Appl1
10	777	44.9	338	4	US-09-303-524A-2 Sequence 3, Appl1
11	677.5	39.1	358	3	US-08-988-876-3 Sequence 3, Appl1
12	505.5	29.2	319	1	US-08-702-344-28 Sequence 28, Appl1
13	365	21.1	361	1	US-08-383-750-4 Sequence 4, Appl1
14	365	21.1	361	3	US-08-352-678-4 Sequence 4, Appl1
15	365	21.1	361	5	PCT-US93-09636-4 Sequence 4, Appl1
16	363.5	21.0	339	1	US-08-153-848-44 Sequence 44, Appl1
17	363.5	21.0	339	2	US-08-812-871-3 Sequence 4, Appl1
18	363.5	21.0	339	3	US-09-299-843A-44 Sequence 44, Appl1
19	363.5	21.0	339	4	US-09-088-337B-44 Sequence 44, Appl1
20	363.5	21.0	339	5	PCT-US93-1153-44 Sequence 44, Appl1
21	363.5	21.0	339	5	PCT-US95-07180-2 Sequence 2, Appl1
22	360.5	20.8	381	1	US-08-467-125-2 Sequence 2, Appl1
23	360.5	20.8	381	2	US-08-911-320A-2 Sequence 2, Appl1
24	360.5	20.8	381	4	US-09-217-101-2 Sequence 2, Appl1
25	359	20.7	348	3	US-08-852-824-17 Sequence 17, Appl1
26	338.5	19.6	337	4	US-09-044-404A-2 Sequence 2, Appl1
27	334.5	19.3	326	1	US-08-118-270-39 Sequence 39, Appl1

28	334.5	19.3	326	5	PCT-US93-08528-39	Sequence 39, Appl1
29	331.5	19.2	342	3	US-08-988-876-9	Sequence 9, Appl1
30	300.5	17.4	358	2	US-08-458-970A-11	Sequence 11, Appl1
31	300	17.3	362	3	US-08-513-974B-374	Sequence 374, Appl1
32	296	17.1	359	1	US-08-148-209A-4	Sequence 4, Appl1
33	295	17.0	400	4	US-09-351-198-2	Sequence 2, Appl1
34	295	17.0	400	4	US-09-113-426-2	Sequence 2, Appl1
35	292.5	16.9	407	2	US-08-742-440A-3	Sequence 3, Appl1
36	292	16.9	400	3	US-08-889-108-8	Sequence 8, Appl1
37	292	16.9	400	4	US-08-188-275A-2	Sequence 2, Appl1
38	292	16.9	400	5	PCT-US94-10358-8	Sequence 8, Appl1
39	291	16.8	370	3	US-08-781-250-2	Sequence 2, Appl1
40	291	16.8	391	2	US-08-454-549-3	Sequence 3, Appl1
41	291	16.8	391	3	US-08-454-552-3	Sequence 3, Appl1
42	291	16.8	398	1	US-08-149-093A-5	Sequence 5, Appl1
43	291	16.8	398	2	US-08-911-245-5	Sequence 5, Appl1
44	291	16.8	398	3	US-08-889-108-2	Sequence 2, Appl1
45	291	16.8	398	4	US-08-120-601B-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-221-456-2
Sequence 2, Application US/09221456
Patent No. 6162899

GENERAL INFORMATION:
APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MUIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS
TITLE OF INVENTION: AND ANTAGONISTS OF THE HNEA81 RECEPTOR
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestlia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/221,456
FILING DATE: 28-DEC-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/956,975
FILING DATE: 23-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestlia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-70318-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0700
TELEX: 846169
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-221-456-2

Query Match 99.7%, Score 1725, DB 4, Length 333;

Best Local Similarity 99.7%; Pred. No. 1.8e-134;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60
    |||
Db 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60

OY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120
    |||
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120

OY 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
    |||
Db 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180

OY 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKLEGVFVVV 240
    |||
Db 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKLEGVFVVV 240

OY 241 AVEFVCFAPFHFARVPYTHSQTNNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
    |||
Db 241 AVEFVCFAPFHFARVPYTHSQTNNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300

OY 301 KKFTEKPCMOGRKTTASSQENHSSQTDNITLG 333
    |||
Db 301 KKFTEKPCMOGRKTTASSQENHSSQTDNITLG 333
```

RESULT 2

US-09-558-740-2
Sequence 2, Application US/09558740
Patent No. 6358695

GENERAL INFORMATION:

APPLICANT: SATHE, GANESH
APPLICANT: HALSEY, WENDY
APPLICANT: MOIR, ALISON
APPLICANT: CHAMBERS, JON
APPLICANT: SZEKERES, PHILIP
TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS OF THE HNEA81 RECEPTOR
FILE REFERENCE: GH-70318-2
CURRENT APPLICATION NUMBER: US/09/558,740
CURRENT FILING DATE: 2000-04-26
PRIOR APPLICATION NUMBER: 08/956,975
PRIOR FILING DATE: 1997-10-23
PRIOR APPLICATION NUMBER: 09/221,456
PRIOR FILING DATE: 1998-12-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSeq for Windows version 3.0
SEQ ID NO 2
LENGTH: 333
TYPE: PRT
ORGANISM: HOMO SAPIENS
US-09-558-740-2

Query Match 99.7%; Score 1725; DB 4; Length 333;
Best Local Similarity 99.7%; Pred. No. 1.8e-134;
Matches 332; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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OY 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60
    |||
Db 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60

OY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120
    |||
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120

OY 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
    |||
Db 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180

OY 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKLEGVFVVV 240
    |||
Db 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKLEGVFVVV 240
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Db 181 GLKWHQVNNICQFIWTVFILMLVEYVVIKAVYDSYRKSCKDRKNNKLEGVFVVV 240

OY 241 AVEFVCFAPFHFARVPYTHSQTNNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
    |||
Db 241 AVEFVCFAPFHFARVPYTHSQTNNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300

OY 301 KKFTEKPCMOGRKTTASSQENHSSQTDNITLG 333
    |||
Db 301 KKFTEKPCMOGRKTTASSQENHSSQTDNITLG 333
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RESULT 3

US-08-812-871-1
Sequence 1, Application US/08812871
Patent No. 595303

GENERAL INFORMATION:

APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl
APPLICANT: Muzong Cheng
TITLE OF INVENTION: NOVEL HUMAN CHEMOKINE RECEPTOR-LIKE
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Dr..
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS

SOFTWARE: FastSeq for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/812,871
FILING DATE: Filed Herewith

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
REGISTRATION NUMBER: 36,749

REFERENCE/DOCKET NUMBER: PF-0237 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 333 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

IMMEDIATE SOURCE:
LIBRARY: MMLR3DT01
CLONE: 568987

US-08-812-871-1

Query Match 98.0%; Score 1697; DB 2; Length 333;
Best Local Similarity 98.5%; Pred. No. 3.6e-132;
Matches 328; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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OY 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60
    |||
Db 1 MNTVMGSENRSEPCPRDRIYQVLEPALYTVFLTGILLNTLALWVHVHIPPSSSTFIY 60

OY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120
    |||
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCVCRFSSVIFETMYGIVLGLIAFDR 120

OY 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
    |||
Db 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
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Db 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFELFISLPIMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQVNNICQFIWTVFILMVFYVIAKKVYDSYRKSCKDRKNNKKLEGKVFVVV 240
Db 181 GLKWHQVNNICQFIWTVFILMVFYVIAKKVYDSYRKSCKDRKNNKKLEGKVFVVV 240
QY 241 AVFFVCAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
Db 241 PVFVCFAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAATNICMDPLIYIFLC 300
QY 301 KFTTEKLPOMGRKTTASSQENHSSQTDNITLG 333
Db 301 KFTTEKLPOMGRKTTASSQENHSSQTDNITLG 333

RESULT 4
US-08-467-948A-6

; Sequence 6, Application US/08467948A
; Patent No. 5998164
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR2
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,948A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-948A-6

Query Match 63.5%; Score 1098.5; DB 2; Length 293;
Best Local Similarity 76.8%; Pred. No. 4.2e-83;
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

QY 1 MNTVMQGFNRSEPCPRDRIVOLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIY 60
Db 1 MNTVMQGFNRSEPCPRDRIVOLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIY 60
QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAVQCRSSVIFYETMYGIVLGLIADFDR 120

Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWQLRAVQCRSSVIFYETMYGIVLGLIADFDR 120
QY 121 FLKIRPLRNIFLKKPVFAKTVSIFWFFELFISLPIMILSNKEATPSSVKKCASLKGPL 180
Db 121 FLKIRPLRNIFLKKPVWGTVSIFWFFEFISLPIMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHQVNNICQFIWTVFILMVFYVIAKKVYDSYRKSCKDRKNNKKLEGKVF--- 237
Db 181 GLKWHQVNNICQFIWTVFILMVFYVIAKKYMLIESPKVTEKTTKSWAKYLLSW 240
QY 238 ---VVAVFFVCAPFHFARVPYTHSQTNKTDCLQNLFIKETTFLAAT 287
Db 241 LSSLCVLLHFTS-PEFHILTVKPTIRLT---VDCKI-NCLLKKQLSFWQOLT 288

RESULT 5
US-08-467-947A-6

; Sequence 6, Application US/08467947A
; Patent No. 6090575
; GENERAL INFORMATION:
; APPLICANT: LI, YI
; APPLICANT: CAO, LIANG
; APPLICANT: NI, JIAN
; APPLICANT: GENTZ, REINER
; APPLICANT: BULT, CAROL J.
; APPLICANT: SUTTON III, GRANGER G.
; APPLICANT: ROSEN, CRAIG A.
; TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
; TITLE OF INVENTION: Coupled Receptor GPR1
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVE., NW, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,947A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04079
; FILING DATE: 30-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: STEFFE, ERIC K.
; REGISTRATION NUMBER: 36,688
; REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 293 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-467-947A-6

Query Match 63.5%; Score 1098.5; DB 3; Length 293;
Best Local Similarity 76.8%; Pred. No. 4.2e-83;
Matches 225; Conservative 14; Mismatches 43; Indels 11; Gaps 4;

QY 1 MNTVMQGFNRSEPCPRDRIVOLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIY 60
Db 1 MNTVMQGFNRSEPCPRDRIVOLVFPALYTVVFLTGILLNTLALWVFVHIPSSSTFIY 60

QY 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGVILGLIAFDR 120
Db 61 LKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGVILGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMILSNKEATPSSVKKASLKGPL 180
Db 121 FLKIIRPLRNIFLKKPVFAKTVSIFIMFLEFISLPNMILSNKEATPSSVKKASLKGPL 180
QY 181 GLKWHOMVNNICQIFETVIFILMLVEFYVIAKKVDSYRKSCKDRKNNKLEGGVF--- 237
Db 181 GLKWHOMVNNICQIFETVIFILMLVEFYVIAKKVDSYRKSCKDRKNNKLEGGVF--- 237
QY 238 ---VVAVFVCFADFEHFAFVRYTHSQTNNKTDCLQNLFIKETTLEAAT 287
Db 241 LSSLCLVLFHIS-PEFHILTVPKPTIRLT---VDCKI-NCLLLKKOLSFMOULT 288

RESULT 6
US-08-852-824-2
Sequence 2, Application US/08852824C
Patent No. 6060272
GENERAL INFORMATION:
APPLICANT: Li et al.
TITLE OF INVENTION: Human G-Protein Coupled Receptors
FILE REFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08/852,824C
CURRENT FILING DATE: 1997-05-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 2
LENGTH: 342
TYPE: PRT
ORGANISM: genomic
US-08-852-824-2

Query Match 47.9%; Score 829; DB 3; Length 342;
Best Local Similarity 49.1%; Pred. No. 6.5e-61;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;
QY 15 CPDRTIRVQLVLPALYTVFELTGLILNTLALWVFIHPPSSSTFIYLNKTLVADLIMT 74
Db 17 CTRDYKIQVLEPLLYTVLFVGLITNGLAMRIEFOIRSKSNFIPLKNTVISDLMLIT 76
QY 75 LPEKILSDSHLAPWOLRAFCRSSVIFETMYGVILGLIAFDRFLKIIRPLRNIFL 134
Db 77 FPEKILSDAKGTGLRFTVCQVTSVIFETMYISISFLGLITDRYQKTRPFTSNPK 136
QY 135 KPVFAKTVSIFIMFLEFISLPNMILSNKEATPSSVKKASLKGPLGLKWHOMVNNICQ 194
Db 137 NLGAKILSVIWAFFMFLSLPMLILNROPDRKNVKKCSFLKSEGLVWHEIVNYICQ 196
QY 195 IFMTVFILMLVEFYVIAKKVDSYRKSCKDRKNNKLEGGVFVAVFVCFAPFHAR 254
Db 197 IFMINEIIVICYTLITKELIRSYVTRGVGVKPRKKVNVKVFIIIAVEFICFVPHFAR 256
QY 255 VPTYHSQTNKTDCLQNLFIKETTLEAATNICMDPLIYIFLCKKFTTEKLPCMQ--G 312
Db 257 IPYTLSDTRDVEFDTAENTLFFYVKESTLWLTSLNACLDPIYFPLCKSFERNLSMLKCP 316
QY 313 RKTASSQENHSSQTD 328
Db 317 NSATSLSQDNRRKKEOD 332

RESULT 7
US-08-467-948A-29
Sequence 29, Application US/08467948A
Patent No. 5998164
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG
APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER

APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,948A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140003/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-948A-29

Query Match 44.9%; Score 777; DB 2; Length 325;
Best Local Similarity 47.5%; Pred. No. 1.1e-56;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;
QY 13 ERCPDRTIRVQLVLPALYTVFELTGLILNTLALWVFIHPPSSSTFIYLNKTLVADLIMT 72
Db 11 ESCSQNLITQIIPVLCMVFIAGILNGVSGWIFFYVPPSSKSFIIYLNKIVIADEVMS 70
QY 73 LMLPEKILSDSHLAPWOLRAFCRSSVIFETMYGVILGLIAFDRFLKIIRPLRNIF 132
Db 71 LTFPEKILGDSGLGPWOLNVEFCVSAVLFVNMVSVIFEGLSFDRIYKIVKPLWTSF 130
QY 133 LKKPVFAKTVSIFIMFLEFISLPNMILSNKEATPSSVKKASLKGPLGLKWHOMVNNIC 192
Db 131 IQSVSYSKLLSVIWMMLLAVPNILITNOSVREVTOIKCIELKSELGRKWHKASNYIF 190
QY 193 QFIFMTVFILMLVEFYVIAKKVDSYRKSCKDRKNNKLEGGVFVAVFVCFAPFHAR 252
Db 191 VAIFMTVFILMLVEFYVIAKKVDSYRKSCKDRKNNKLEGGVFVAVFVCFAPFHAR 250
QY 253 ARVPTYHSQTNKTDCLQNLFIKETTLEAATNICMDPLIYIFLCKKFTTEKL 307
Db 251 ARIPYTSQTEAHYSCQSKELIRYKKEFTLLLSAANVCLDPIYFPLCKSFERNLSMLKCP 305

RESULT 8
US-08-467-947A-29
Sequence 29, Application US/08467947A
Patent No. 6090575
GENERAL INFORMATION:
APPLICANT: LI, YI
APPLICANT: CAO, LIANG

APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: BULT, CAROL J.
APPLICANT: SUTTON III, GRANGER G.
APPLICANT: ROSEN, CRAIG A.
TITLE OF INVENTION: Polynucleotides Encoding Human G-Protein
TITLE OF INVENTION: Coupled Receptor GPR1
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVE., NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,947A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04079
FILING DATE: 30-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1140002/EKS/KLM
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
US-08-467-947A-29

Query Match 44.9%; Score 777; DB 3; length 325;
Best Local Similarity 47.5%; Pred. No. 1.1e-56;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;
QY 13 ERCPDTRIVQVLPALYTVVFLTGILNTLALWVFWHIPSSSTFIYLYKNTLVADLMT 72
DB 11 ESCSONLLITQIIPVLYCMVFIAGILLNGVSGWIFFYVSSKSFIIYLYKNIVADFWMS 70
QY 73 LMLPEKILSDSHLAPWQRAFCRVSSVIFETMYVGIIVLLGLIAFDRFLKIRPLRNIF 132
DB 71 LTFPEKILGDSGLGPWQNVFCRVSAVLFYVNMVYSIVFEGGLISFIRYKIVKPLMTSF 130
QY 133 LKKPVFAKTVSIFWIFELFISLPNMLSNKEATPSSVKKCASLKGFLGKWHQVNNIC 192
DB 131 IQSVSYSKLSLVYVMMMLLAVPNIILTNQSVREYTOIKCIELKSELGRKWHKASNYIF 190
QY 193 QFIWTVFILMLVFYVVIKAKVYDSYRKSRSKDRKNNKKLEGKVFAVAVFVCFAPFHF 252
DB 191 VAIWFIVFLLIVFYTAITKKIFKSHLKSRSNSTSVKKSRRNIFSIVFVFCFVPHYI 250
QY 253 ARVPYTHSQTNNKTDCLONQFLIAKETTLFLAATNICMDPLIYIFLCKKFEKTL 307
DB 251 ARIPYTKSQTEAHYSQSKELIRYKMEFTLLLSAANVCLDPIITYFFLCQPREIL 305

RESULT 9
US-08-988-876-8
Sequence 8, Application US/08988876
Patent No. 6063596
GENERAL INFORMATION:

APPLICANT: Lal, Preeti
APPLICANT: Bandman, Olga
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
TITLE OF INVENTION: WITH IMMUNE RESPONSE
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 285995
US-08-988-876-8

Query Match 44.9%; Score 777; DB 3; length 338;
Best Local Similarity 47.5%; Pred. No. 1.2e-56;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;
QY 13 ERCPDTRIVQVLPALYTVVFLTGILNTLALWVFWHIPSSSTFIYLYKNTLVADLMT 72
DB 12 ESCSONLLITQIIPVLYCMVFIAGILLNGVSGWIFFYVSSKSFIIYLYKNIVADFWMS 71
QY 73 LMLPEKILSDSHLAPWQRAFCRVSSVIFETMYVGIIVLLGLIAFDRFLKIRPLRNIF 132
DB 72 LTFPEKILGDSGLGPWQNVFCRVSAVLFYVNMVYSIVFEGGLISFDRYKIVKPLMTSF 131
QY 133 LKKPVFAKTVSIFWIFELFISLPNMLSNKEATPSSVKKCASLKGFLGKWHQVNNIC 192
DB 132 IQSVSYSKLSLVYVMMMLLAVPNIILTNQSVREYTOIKCIELKSELGRKWHKASNYIF 191
QY 193 QFIWTVFILMLVFYVVIKAKVYDSYRKSRSKDRKNNKKLEGKVFAVAVFVCFAPFHF 252
DB 192 VAIWFIVFLLIVFYTAITKKIFKSHLKSRSNSTSVKKSRRNIFSIVFVFCFVPHYI 251
QY 253 ARVPYTHSQTNNKTDCLONQFLIAKETTLFLAATNICMDPLIYIFLCKKFEKTL 307
DB 252 ARIPYTKSQTEAHYSQSKELIRYKMEFTLLLSAANVCLDPIITYFFLCQPREIL 306

RESULT 10
US-09-303-524A-2
Sequence 2, Application US/09303524A

```
; Patent No. 6238873
; GENERAL INFORMATION:
; APPLICANT: CHAMBERS, JONATHAN K.
; APPLICANT: STEWART, BRIAN R.
; APPLICANT: AMES, ROBERT S.
; APPLICANT: SARAU, HENRY M.
; APPLICANT: FOLEY, JIM
; APPLICANT: ARNOLD, ANNE ROMANIC
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN THE HUMAN KIAA0001
; TITLE OF INVENTION: RECEPTOR AND LIGANDS THEREOF
; FILE REFERENCE: GP50007
; CURRENT APPLICATION NUMBER: US/09/303,524A
; CURRENT FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,957
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-303-524A-2
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Query Match 44.9%; Score 777; DB 4; Length 338;
Best Local Similarity 47.5%; Pred. No. 1.2e-56;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;
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QY 13 ERCPDRTRIVOLVLPALTYVFLTGILNTLALWVHVHPPSSSTFIYLNKTLVADLIMT 72
DB 12 ESCSONLITFOQIIFVLYCMVFAGILNGVSGWIFVYPSKSFIIYLNKNIIVADFVMS 71
QY 73 LMLPKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIYLLGLAEDRFLKIIRPLRNIF 132
DB 72 LTFPKILGDSGLPWLNVFCVRSVAVLYVNMVSVIVFGLISFDRIYKIVKPLWTSF 131
QY 133 LKKPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKCAELKGPLGLKWHOMVNNIC 192
DB 132 IQSVSYSKLSLVYVMMMLLAVPNIILNOSVREVTOIKCIELKSELGRKWHKASNYIF 191
QY 193 QFIFWVFILMLVYVVIKAVYDSYRSKSKDRKNNKLEGVAVVAVVAVFVCFAPFHF 252
DB 192 VAFWVIFLLLVFYTAITKIKFKSHKSSRNSTSVKKSRRNIFSVFVFCVVPYHI 251
QY 253 ARVPYTHSQNNKTDCLQNLQFLAKETTLFLAATNICMDPLIYIFLCKKTEKL 307
DB 252 ARIPTYKQTEAHYSCOSKEILRYMKEFTLLLSAANVCLDPIIYFELCQPFREIL 306
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RESULT 11

```
US-08-988-876-3
; Sequence 3, Application US/08988876
; Patent No. 6063596
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Bandman, Olga
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Yue, Henry
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTORS ASSOCIATED
; TITLE OF INVENTION: WITH IMMUNE RESPONSE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
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SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/988,876
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0441 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: PROSTUT09
CLONE: 1650519
; US-08-988-876-3
```

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Query Match 39.1%; Score 677.5; DB 3; Length 358;
Best Local Similarity 40.7%; Pred. No. 1.8e-48;
Matches 124; Conservative 69; Mismatches 101; Indels 11; Gaps 3;
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QY 10 NRSECPDRTRIVQ---LVFPALTYVFLTGILNTLALWVHVHPPSSSTFIYLNKTL 65
DB 25 NRSDBGKNTILNEDFTIVLPVLYLIFVASILLGLAVWIFPHIRNKTSFIYLNKIV 84
QY 66 VADLIMTLMPFKILSDSHLAPWQLRAFCVCRSSVIFYETMYVGIYLLGLAEDRFLKII 125
DB 85 VADLIMTLTPFRIVHDAGFGPWYFKFICRYTSVLFYANMTYSIVFGLISIDRYLKVV 144
QY 126 RPLRNIFLKKPVFAKTVSIFWFLFISLPMILSNKEATPSSVKKCASIKGPLGLKWH 185
DB 145 KPEGDSRMYSITFTKVLSCVWVIMAVLSLPIILNLTNGOPTEDNIDCSKPLGVKWH 204
QY 186 QMWNNICQFIFWVFILMLVYVVIKAVYDSYRK--SKSKDRKNNKLEGKVFVVAV 242
DB 205 TAVTYVNSCLPVAVLVILGCIYAIISRYIHKSSRQFISOSSRRKKNQSTR---VVAV 260
QY 243 FVCFAPFHFARVPYTHSQNNKTDCLQNLQFLAKETTLFLAATNICMDPLIYIFLCKK 302
DB 261 YFTCFLPYHLCRMPSTFSLDRLDDESAOKILYYCKEITLFLSACNVCIDPIIYFEMCRS 320
QY 303 FTEKL 307
DB 321 FSRWL 325
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RESULT 12

```
US-08-702-344-28
; Sequence 28, Application US/08702344
; Patent No. 5723315
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John
; APPLICANT: Lavallee, Edward
; APPLICANT: Racle, Lisa
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
```

STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/702,344
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 319 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-344-28

Query Match 29.2%; Score 505.5; DB 1; Length 319;
Best Local Similarity 33.4%; Pred. No. 2.1e-34;
Matches 107; Conservative 64; Mismatches 134; Indels 15; Gaps 5;
QY 10 NRSEPCP--RDRIVQLVLPALYTVFELTGILNLTALMVEVHIPSSSTFI-ITLKNTLV 66
DB 3 NSSFCFVYKDE----PFTYFYLVLVGLIGSCFATWAFIOKNTNARCVSITLNLIT 58
QY 67 ADLIMTLMPEKILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDRLKIIR 126
DB 59 ADFLLTLALPVKIVVDLGVAPWKLIKHCQVTACLIYINMYLSIIFLAFAVSIDRCIQTH 118
QY 127 PLRNIFLKKPVFAKTVSIFIFWFLFISLPNMLISNKEATPSSVKKCASLKGDLGKWHQ 186
DB 119 SCKIYRIQEPGFAMISTVWMLVLLIMVPMNIPKIDIKESNVGCMFKKEGRNWHL 178
QY 187 MVNNICQIFWTFEILMVEYVIAKKVDSYRKSCKDKRNKKLEKVFVYAVFEVC 246
DB 179 LTNFICVAFILNESAIIILSNCLVIRQL--YRNKDNNENYPNVKKALINILVTGYYIC 235
QY 247 FAPFHARVPYTHSQTNKTCRLQNLQLEIAKETTLFLAATNICMDPLIYIFLCKKFTK 306
DB 236 FVPYHIVRIPTLSQTEVITDCSTRISLEKRAEATLLAVSNLCFDPILYYHLSKAFRSK 295
QY 307 LPCMGKRTTASSQENHSSQ 326
DB 296 V-----TETFPASPKETKAOK 310

RESULT 13
US-08-383-750-4
Sequence 4, Application US/08383750
Patent No. 5744301
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
CITY: Washington
STATE: D.C.

COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627.3300001.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-383-750-4

Query Match 21.1%; Score 365; DB 1; Length 361;
Best Local Similarity 27.2%; Pred. No. 8.3e-23;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;
QY 23 QLVFPALYTVFELTGILNLTALMVEVH---IPSSSTFIITLKNTLVADLIMTLMPEK 78
DB 31 RIVMPLHYSLVFLIGLVGNLALVIVQNRKKINSTT--LYSTNLVISDILFTYALPTR 87
QY 79 ILSDSHLAPWOLRAFCRSSVIFETMYGIVLLGLIAFDRLKIIRPLRNIFLKKPV 138
DB 88 IAYVAMGEDWRIGDALCRITALEVYINTYAGVNFMTGLSIDRFIAVHPLRYNRIKRIE 147
QY 139 AKTVSIFIFWFLFISLPNMI--LSNKEATPSSVKKCASLKGDLGKWHQMVNNICQFIF 196
DB 148 AKGVCIWFVILVFAQTPLILINPMASKQEAERITCMEYFNFEETKSLPW--ILGACFICY 205
QY 197 WTVFILMVEYVIAKKVDSYRKSCKDRKN--NKKLEKGVFVYAVFEVCAPFHARV 255
DB 206 VLPILIIILICYSQICCKLFTAKONPLTEKSGVKNKALNTIILIVFVLCFTPYHVAII 265
QY 256 PYTHSQT--NKTDCRLQNLQLEIAKETTLFLAATNICMDPLIYIFLCKKFTKPCMGQR 313
DB 266 QHMIKKLRFSNFLECSQHSFOISLHFTVCLMNFNCMDPFIYFACKGYKRYMRLKR 325
QY 314 KTAS-----SQENHSSQTD 328
DB 326 QVSVSISAVKSAPEENSREMT 348

RESULT 14
US-08-352-678-4
Sequence 4, Application US/08352678
Patent No. 6043351
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/352,678
FILING DATE: 30-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/980,518
FILING DATE: 25-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: B0801/7044
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-352-678-4

Query Match 21.1%; Score 365; DB 3; Length 361;
Best Local Similarity 27.2%; Pred. No. 8.3e-23;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

QY 23 QLVFPALYTVVFLTGILNTLALWVEVH----IPSSSTFIYLYKNTLVADLIMTLMLPK 78
DB 31 RIVMPLHYSLVFLIGLVNLLALVIVONRKKINST--LYSTNLVISDILEFTTALPTR 87
QY 79 ILSDSLAPWQLRAFCRESSVIFYETMYVGIYLLGLIAFDRFLKIIRPLRNIFLKKPVF 138
DB 88 IAYYAMGFDMRIGALCRITALVFIYNTYAGVNMTCLSIDRFIAVVPRLRYNKKIRIEH 147
QY 139 AKTVSIFWFLFELFISLPNMI--LSNKEATPSSVKKCASLKGPLGLKWHQVNNICQFIF 196
DB 148 AKGVCIFWILVFAQTLPPLINPMSKQEAERITCMEYPNFEETKSLPW--ILGACFIGY 205
QY 197 WTVFILMLVFYVIAKKVYDSYRKSCKDRKN-NKKLEGKVFVVAVEFCFAPHFARV 255
DB 206 VLPLIILICYSOICCKLFTAKONPLTEKSGVNNKALNTIILIVVFVLCFTPYHVAII 265
QY 256 PYTHSQT--NNKTDCLQNLQFLIAKETTLFLAATNIDMDPLIYIFLCKKTEKLPQMGR 313
DB 266 OHMIKKLRFNSNLECSORHSFQISLHFTVCLMNFNCMDPFIYFFACKGYKRVKVMRLKR 325
314 KTAS-----SQENHSSQTD 328
DB 326 QVSVSISAVKSAPENSREMT 348

RESULT 15
PCT-US93-09636-4
Sequence 4, Application PC/TUS9309636
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Kieff, Elliot
TITLE OF INVENTION: Epstein Barr Virus Induced Genes
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue N.W., Suite 600
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09636
FILING DATE: herewith
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
PCT-US93-09636-4

Query Match 21.1%; Score 365; DB 5; Length 361;
Best Local Similarity 27.2%; Pred. No. 8.3e-23;
Matches 88; Conservative 78; Mismatches 135; Indels 22; Gaps 7;

QY 23 QLVFPALYTVVFLTGILNTLALWVEVH----IPSSSTFIYLYKNTLVADLIMTLMLPK 78
DB 31 RIVMPLHYSLVFLIGLVNLLALVIVONRKKINST--LYSTNLVISDILEFTTALPTR 87
QY 79 ILSDSLAPWQLRAFCRESSVIFYETMYVGIYLLGLIAFDRFLKIIRPLRNIFLKKPVF 138
DB 88 IAYYAMGFDMRIGALCRITALVFIYNTYAGVNMTCLSIDRFIAVVPRLRYNKKIRIEH 147
QY 139 AKTVSIFWFLFELFISLPNMI--LSNKEATPSSVKKCASLKGPLGLKWHQVNNICQFIF 196
DB 148 AKGVCIFWILVFAQTLPPLINPMSKQEAERITCMEYPNFEETKSLPW--ILGACFIGY 205
QY 197 WTVFILMLVFYVIAKKVYDSYRKSCKDRKN-NKKLEGKVFVVAVEFCFAPHFARV 255
DB 206 VLPLIILICYSOICCKLFTAKONPLTEKSGVNNKALNTIILIVVFVLCFTPYHVAII 265
QY 256 PYTHSQT--NNKTDCLQNLQFLIAKETTLFLAATNIDMDPLIYIFLCKKTEKLPQMGR 313
DB 266 OHMIKKLRFNSNLECSORHSFQISLHFTVCLMNFNCMDPFIYFFACKGYKRVKVMRLKR 325
314 KTAS-----SQENHSSQTD 328
DB 326 QVSVSISAVKSAPENSREMT 348

Search completed: October 11, 2002, 14:50:57
Job time : 20 secs


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FT DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 299 7 (POTENTIAL).
FT DOMAIN 300 338 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 338 AA; 38971 MW; 8DBEC782CB4753D CRC64;

Query Match 44.9%; Score 777; DB 1; Length 338;
Best Local Similarity 47.5%; Pred. No. 1e-41;
Matches 140; Conservative 54; Mismatches 101; Indels 0; Gaps 0;

OY 13 ERCPDRTRIQVLPALYVVELFGILNTLALWVPHIPSSSTFIYLNKTLVADLMT 72
DB 12 ESCSQNLLITQOIIPLVLCMVFIAGILNGVSGWIFVPSKSFIIYLNKIVIADEFMS 71
OY 73 LMLPKILSDSHLAPWQLRAFCRVSSVIFETMYGVLLGLAFDRFLKIRPLRNIF 132
DB 72 LTFPKILGDSGLPWLNVFCRVSAVLFYVMYVSIYFGLISFDRIYKIVKPLMTSF 131
OY 133 LKKPVFAKVSIFWELFISLPNMLSNKEATPSSVKKCA:LGKPLGLKWHQVNNIC 192
DB 132 IQSVSYSKLSYIVWMLLAVPNILITNSVREVTOIKCIHLKSELGRKWKASNYIF 191
OY 193 QEIFWTFILMLVEYVVIKAVYDSYRSKSKDRKNNKLEGVYVAVFVFCAPFHF 252
DB 192 VAFWVIFLLVLYFYTAITKKIKFSLKSSRNSTSVKSSRNIFSVFVFCVPIYHI 251
OY 253 ARVPYTHSQTNKTDCLQNLQFLAKETTLFLAATNICMDPLVIFLCKKFTKEL 307
DB 252 ARIPTYKQTEAHYSCQSKELRYMKEFTLLLSAANCVDPIYFFLCQPFREIL 306

RESULT 2
KI01_RAT STANDARD; PRT; 305 AA.
ID KI01_RAT
AC 035881;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Probable G protein-coupled receptor VTR 15-20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Charlton M.E., Williams A.S., Fogliano M., Sweetnam P.M., Duman R.S.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: ORPHAN RECEPTOR.
-1- SUBCELLULAR LOCATION: Integral membrane protein.
-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
PROBABLE ORTHOLOG OF HUMAN KIAA0001.
-----
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CC or send an email to license@isb-sib.ch).
-----
CC EMBL: U76206; AAB71745.1; -
CC GCRDB: GCR_2520; -
CC InterPro: IPR000276; GPCR_Rhodpsn.
CC Pfam: PF00001; 7tm_1; 1.
DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; FALSE_NEG.
DR PROSITE: PS50262; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 29 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 30 50 1 (POTENTIAL).
FT DOMAIN 51 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 76 2 (POTENTIAL).
FT DOMAIN 77 96 EXTRACELLULAR (POTENTIAL).

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FT TRANSMEM 97 117 3 (POTENTIAL).
FT DOMAIN 118 139 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 140 160 4 (POTENTIAL).
FT DOMAIN 161 188 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 189 209 5 (POTENTIAL).
FT DOMAIN 210 234 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 235 255 6 (POTENTIAL).
FT DOMAIN 256 278 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 279 299 7 (POTENTIAL).
FT DOMAIN 300 305 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 305 AA; 34800 MW; 640646A68ECC7A3 CRC64;

Query Match 41.2%; Score 713; DB 1; Length 305;
Best Local Similarity 44.4%; Pred. No. 8.6e-38;
Matches 130; Conservative 57; Mismatches 104; Indels 2; Gaps 1;

OY 2 NTTVMQGFNSRCPDRTRIQVLPALYVVELFGILNTLALWVPHIPSSSTFIY 61
DB 3 NTTTTE--PKQPCRTNRLITQOIIPLVCYVFITGVLLNGISGWIFVPSKSFIIYL 60
OY 62 KNTLVADLITMLPKILSDSHLAPWQLRAFCRVSSVIFETMYGVLLGLIAFDRE 121
DB 61 KNIVVADFNLGLTFEPKVLSDSGLPWLNVFVRSAVIFYVMYVSAIEFGLISFDY 120
OY 122 LKIIRPLRNIFLKKPVFAKVSIFWELFISLPNMLSNKEATPSSVKKCA:SLKGPLG 181
DB 121 YKIVKPLVLSIVQSVNSKLSVLMVWMLLAVPNILITNSVKDVTNIQCMELKNELG 180
OY 182 LKWHQVNNICQEIFWTFILMLVEYVVIKAVYDSYRSKSKDRKNNKLEGVYVVA 241
DB 181 RKWHKASNYVFSIFWIFLLTVFYMATIRKIKFSLKSSRNISVYKSSRNIFSVL 240
OY 242 VEFVFCAPFHFARVPYTHSQTNKTDCLQNLQFLAKETTLFLAATNICMDPL 294
DB 241 AFWACFAPYHVARIPYTKSQTEGHYSCQAKETLLTYKFTLLLSAANCVDPI 293

RESULT 3
H963_HUMAN STANDARD; PRT; 319 AA.
ID H963_HUMAN
AC 014626;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor H963.
GN H963.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Peripheral blood monocytes;
RX MEDLINE-98036061; PubMed-9370294;
RA Jacobs K.A., Collins-Racie L.A., Colbert M., Duckett M.,
RA Golden-Fleet M., Kelleher K., Ritz R., Lavallie E.R., Merberg D.,
RA Spaulding V., Stover J., Williamson M.J., McCoy J.M.;
RT "A genetic selection for isolating cDNAs encoding secreted proteins.";
RL Gene 198:289-296(1997).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
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DR EMBL; AF002986; AAC51846.1; -
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 21 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 22 42 1 (POTENTIAL).
FT DOMAIN 43 48 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 49 69 2 (POTENTIAL).
FT DOMAIN 70 89 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 90 110 3 (POTENTIAL).
FT DOMAIN 111 132 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 133 153 4 (POTENTIAL).
FT DOMAIN 154 181 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 182 202 5 (POTENTIAL).
FT DOMAIN 203 224 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 225 245 6 (POTENTIAL).
FT DOMAIN 246 268 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 269 289 7 (POTENTIAL).
FT DOMAIN 290 319 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 3 3 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 319 AA; 36754 MW; 79B9821C10841114 CRC64;

Query Match
Best Local Similarity 29.2%; Score 505.5; DB 1; Length 319;
Matches 107; Conservative 33.4%; Pred. No. 5,7e-25;
Mismatches 134; Indels 15; Gaps 5;

OY 10 NRSEKCP--RDRTRIVQLVLPALYTVFELTGLNTLALWVFIHPSSTFI-IYLNKTLV 66
DB 3 NSSFCFVYKDE----PFTYFYLVLVGLIGSCFATWAFIQKNTNHRCSVLYLNLIT 58
OY 67 ADLIMTLMPEKILSDSHLAPWQLRAFCVCFSSVIFETWYVGIIVLGLIAFDRLKTIIR 126
DB 59 ADELTLALPVKIVDVGAPWKLKIFHCQVACLIYINMYLSTIFIAFVSIDRCIQLTH 118
OY 127 PLRNIFLKKPVFAKTVSIFWFFLFISLPNMTISNKEATPSSVKKCASLKGPLGKWHQ 186
DB 119 SKTIYRIQEPGPAKMISTVWMLVLLIMVPMIPKIDIKESNVGCMFEKFERGNMHL 178
OY 187 MVNNICQIFETWVFIIMLVFYVIAKKVDSYRSKSKDRKNNKLEGVFVVAVEFVC 246
DB 179 LTNFICVAIFLNSAILISNCLVIRQL--YRNKDENEYPNVKKALINILLYTTGYIIC 235
OY 247 FAFHFARVPYTHSQTNKNTDCLRNQLFIKETTLELATNLCMDFLIYFLCKKTEK 306
DB 236 FVPYHIVRIPTYLSQTEVITDCSTRISLFAKKEATLLAVSNLCFDFILYHLSKAFRSK 295
OY 307 LPCMGRKTTASSQENHSSQ 326
DB 296 V-----TEFASPKETKAQK 310

RESULT 4
GPRY_MOUSE STANDARD; PRT: 375 AA;
ID GPRY_MOUSE
AC Q9RIK6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schulz A., Grosse R., Schade R., Henzlajn P.,
RA Schultz G., Gudermann T.;
RT "A novel subgroup of class I G-protein-coupled receptors.";
```

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RL Blochim. Biophys. Acta 1446:57-70(1999).
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF081916; AAD50550.2; -
DR MGI; MGI:1346334; Gpr34.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 54 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 55 75 1 (POTENTIAL).
FT DOMAIN 76 81 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 82 102 2 (POTENTIAL).
FT DOMAIN 103 121 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 122 142 3 (POTENTIAL).
FT DOMAIN 143 164 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 165 185 4 (POTENTIAL).
FT DOMAIN 186 209 5 (POTENTIAL).
FT TRANSMEM 210 230 6 (POTENTIAL).
FT DOMAIN 231 262 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 263 283 7 (POTENTIAL).
FT DOMAIN 284 303 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 304 324 7 (POTENTIAL).
FT DOMAIN 325 375 CYTOPLASMIC (POTENTIAL).
FT DISULFID 120 197 BY SIMILARITY.
FT CARBOHYD 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 29 29 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 35 35 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 193 193 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 375 AA; 43173 MW; C04E1C1A52521045 CRC64;

Query Match
Best Local Similarity 22.7%; Score 392.5; DB 1; Length 375;
Matches 97; Conservative 29.1%; Pred. No. 6,2e-18;
Mismatches 149; Indels 21; Gaps 8;

OY 15 CPRDTRIVQLVLPALYTVFELTGLNTLALWVFIHPSSTFI-IYLNKTVADLIMTL 73
DB 39 CPMDEKLLSTVLTTFYSVFLVGLVGNILALYFLGIHRKRNISQIYLLNVAADLLIF 98
OY 74 MLPKILSDSHLAPWQLRAFCVCFSSVIFETWYVGIIVLGLIAFDRLKTIIRPL---RN 130
DB 99 CLPERIMYHINONKMTGLVILCKVGTFLFYMMYISILLGFIISLDRIYKINSIQORRA 158
OY 131 IFLKKPVFAKTVSIFWFFLFISLPNMTLSNKEATPSSVKKCASLKGPLGKWHQVNN 190
DB 159 ITTKOSIY---VCCIVWTVVALAGFLTMIILTKKGHNST-MCFHYRDRHNAKGEAIFNF 214
OY 191 ICQIFWTVFIMLVFYVIAKKVD-SYRSKSKDRKNNKLEGVFVVAVEFVCFAP 249
DB 215 VLVMFWLIFLLIISYIKIGKNLIRISKRSKPEPNSGYATTARNSEFLVLIITICFVP 274
OY 250 FHFARVPYTHSQTNKNTDCLRNQLFIKETTLELATNLCMDPLIYFLCKKTEKLP 309
DB 275 YHAFREYISSL-NVSSCYWKEIHKTNELMLVESSFNSCLDPVMY-FLMSSNIRKIMC 332
OY 310 M-----GGRKTTASSQENHSSQFDNITL 332
DB 333 QLLFRFRQSEASRSESTSEKPGHSLHLSVTV 365
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RESULT 5
GPRY_HUMAN
ID GPRY_HUMAN STANDARD; PRT; 381 AA.
AC O9UPC5; 095853;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Probable G protein-coupled receptor GPR34.
GN GPR34.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Fetal brain;
RX MEDLINE=99326137; PubMed=10395919;
RA Schoneberg T., Schulz A., Grosse R., Schade R., Henklein P.,
RA Schultz G., Gudermann T.;
RT "A novel subgroup of class I G-protein-coupled receptors.";
RL Biochim. Biophys. Acta 1446:57-70(1999).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99156852; PubMed=10036181;
RA Marchese A., Sawzdargo M., Nguyen T., Cheng R., Heng H.H., Nowak T.,
RA Im D.-S., Lynch K.R., George S.R., O'Dowd B.F.;
RT "Discovery of three novel orphan G-protein-coupled receptors.";
RL Genomics 56:12-21(1999).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20434921; PubMed=10982042;
RA Jacobl F.K., Broghammer M., Pesch K., Zrenner E., Berger W.,
RA Meindl A., Pusch C.M.;
RT "Physical mapping and exclusion of GPR34 as the causative gene for
RT congenital stationary night blindness type 1.";
RL Hum. Genet. 107:89-91(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,
RA Tanase T., Nomura Y., Togiyasu S., Komai F., Hara R., Takeuchi K.,
RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,
RA Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Oshima A.;
RT "NEDO human cDNA sequencing project.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: ORPHAN RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- TISSUE SPECIFICITY: BROADLY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC -----
CC EMBL; AF039686; AAD50531.1; -
CC EMBL; AF118670; AAD17248.1; -
CC EMBL; AK027780; BAB55362.1; -
CC MIM; 300241; -
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC Receptor; G-protein coupled receptor; Transmembrane; Glycoprotein.
CC DOMAIN 1 61 EXTRACELLULAR (POTENTIAL).
CC TRANSMEM 62 82 1 (POTENTIAL).
CC DOMAIN 83 88 CYTOPLASMIC (POTENTIAL).

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FT TRANSMEM 89 109 2 (POTENTIAL).
FT DOMAIN 110 128 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 129 149 3 (POTENTIAL).
FT DOMAIN 150 171 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 172 192 4 (POTENTIAL).
FT DOMAIN 193 216 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 217 237 5 (POTENTIAL).
FT DOMAIN 238 269 6 (POTENTIAL).
FT TRANSMEM 270 290 7 (POTENTIAL).
FT DOMAIN 291 310 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 311 331 7 (POTENTIAL).
FT DOMAIN 332 381 CYTOPLASMIC (POTENTIAL).
FT DISULFID 127 204 BY SIMILARITY.
FT CARBOHYD 28 28 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 200 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 295 295 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 181 181 L -> V (IN REF. 1).
SQ SEQUENCE 381 AA; 43860 MW; 491FC0165624379 CRC64;

Query Match
Best Local Similarity 22.6%; Score 391.5; DB 1; Length 381;
Matches 95; Conservative 63; Mismatches 141; Indels 17; Gaps 8;

OY 15 CPRDTRIVOLVLPALTYVFLTGILNTLALWVFIHPSSTFI-IYLNKTLVADLIMTL 73
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 46 CPMDEKLSIYLTSTYSYVIFVGLVGNITIALYVFLGIHRKRNSIQIYLLNVAIADLLIF 105
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

OY 74 MLPFKILSDSHLAPWOLRAFCVCRFSYVIFETWYVGIIVLLGLIAFDRLKIIRPLRN-- 130
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 106 CLPFRIMYHINQNKWTLGLVILCKVGVFLFYNNYISITLLGLFISLDRIYIKINRSIQORKA 165
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

OY 131 IFLKKPVEAKTVSIFWFFFLFISLPNMLISNKEATPSSVKKCASLGLKWKHOMVNN 190
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 166 ITTKQSIY---VCCIVMLALGFLFMILITLKKGGHNSI-MCFHYDKHNAKEAIFNF 221
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

OY 191 ICQFIPTVFIIMLVFYVIAKKVVD-SYRKSXSKDRKNNKLEGVVAVFVCFAP 249
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 222 ILVVMFNLIFLLILSYIKIGKNLIRISKRSPNSGKYATATARNSEFVLIIFTICFVP 281
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

OY 250 FHFARVPYTHSQTNKTDCLQNLQFLAKETTLFLAATNICMPLIYIFLCKFTKLP 309
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 282 YHAFRFYIISQL-NVSSCYWKEIVKHTNEIMLVLSFNSCLDPVMT-FLMSSNIRKIMC 339
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

OY 310 -----MOGRKTPASS 319
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11
Db 340 QLLFRFRQGEPSRSES 355
   11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11 11

RESULT 6
EBI2_HUMAN
ID EBI2_HUMAN STANDARD; PRT; 361 AA.
AC P32249;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE EBV-induced G protein-coupled receptor 2 (EBI2).
GN EBI2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93188173; PubMed=8383238;
RA Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
RA Kieff E.;
RT "Epstein-Barr virus-induced genes: first lymphocyte-specific G
RT protein-coupled peptide receptors.";
RL J. Virol. 67:2209-2220(1993).
CC -1- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
CC LYMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.

```


Best Local Similarity 27.7%; Pred. No. 3.5e-16;
Matches 90; Conservative 69; Mismatches 137; Indels 29; Gaps 9;

QY 12 SERCPDRTRIVOLVPPALYTVFVLGTGLTLALWVFWHPISST-FIYKNTLVADLI 70
DB 20 AEQCGOETPLENMFASFYLLDFILALVGNLMLFIRDHKSSTPANVFLMHLAVADLS 79

QY 71 MTMLPFKIL---SDSHLAPWQLRAVCRFSVIFETMYGVGLGLAFDRFLKIIRP 127
DB 80 CVLVLPRLVYHFGSNH---WPGELACRLTGLFYLNMVASYFLTCISADRLAIVHP 136

QY 128 LRNIFLKKPVEAKTVSIFWFFLFIPLNMLISNKEATPSSVKKCASLKGPLGLKWHOM 187
DB 137 VKSLKLRRLPLVLAHACAFLM-VVAVAMAPLIVSPQTQVTHVVCLOLYREKA-SHAL 194

QY 188 VNNICQFIWVFIILVFIYVIAKKVYSYRSKSKDRKNNKLEGVFVVAVFVCF 247
DB 195 VSLAVAFTE--PITTVTCYLLIR---SLRQGLRVEKRLKVKAVRMIAIVLAIFLVCF 248

QY 248 APFHARVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIFLCKKFTKEL 307
DB 249 VPYHVNRSVYVLYHRSHGASCATQRIALANRITSCLTSLNGALDPIMTFVFAEKFRHAL 308

QY 308 -----PCMQRKTTASS 319
DB 309 CNLCCGKRLKGPPSPFEG-KTNESS 332

RESULT 8
CLUT1_HUMAN STANDARD; PRT; 337 AA.
AC Q9Y271;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4 receptor) (LTD4 receptor) (HG55) (HMTMF81).
GN CysLTR1 OR CysLTR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Tonsil;
RX MEDLINE=99318129; PubMed=10391245;
RA Lynch K.R., O'Neill G.P., Liu Q., Im D.-S., Sawyer N., Metters K.M., Coulombe N., Abramovitz M., Figueroa D.J., Zeng Z., Connolly B.M., Bai C., Austin C.P., Chateaufort A., Stocco R., Greig G.M., Kargman S., Hooks S.B., Hosfield E., Williams D.L. Jr., Ford-Hutchinson A.W., Caskey C.T., Evans J.F.;
RA "Characterization of the human cysteinyl leukotriene CysLTR1 receptor."
RT Nature 399:789-793(1999).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE-Peripheral blood monocytes, leukocyte, and Spleen;
RX PubMed=10462554;
RA Sarau H.M., Ames R.S., Chambers J., Ellis C., Elishourbagy N., Foley J.J., Schmidt D.B., Muccitelli R.M., Jenkins O., Murdock P.R., Herity N.C., Halsey W., Sathie G., Muir A.I., Nuthalaganti P., Dytko G.M., Buckley P.T., Wilson S., Bergsma D.J., Hay D.W.P.;
RA "Identification, molecular cloning, expression, and characterization of a cysteinyl leukotriene receptor."
RT Mol. Pharmacol. 56:657-663(1999).
RL [1]
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating bronchoconstriction of individuals with and without asthma. Stimulation by LTD4 results in the contraction and proliferation of smooth muscle, edema, eosinophil migration and damage to the mucus layer in the lung. This response is mediated via a G-protein that activates a phosphatidylinositol-calcium second messenger system. The rank order of affinities for the leukotrienes is LTD4 >> LTE4 - LTC4 >> LTB4.

CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: Widely expressed, with highest levels in spleen and peripheral blood leukocytes. Lower expression in several tissues, such as lung (mostly in smooth muscle bundles and alveolar macrophages), placenta, small intestine, pancreas, colon and heart.
CC -1- MISCELLANEOUS: Selective antagonists, such as montelukast (Singulair), zafirlukast (Accolate) and pranlukast (Onon), are used in the treatment of the asthma crisis.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.

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CC EMBL; AF119711; AAD42285.1; -
CC EMBL; AF133266; AAD42778.1; -
CC MIM; 300201; -
CC HSSP; P34996; 1DD.
CC InterPro; IPR004071; Cysleuk_receptor.
CC InterPro; IPR00276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR01533; CysLTRRECEPT.
CC PRINTS; PR00237; GPCR_Rhodopsin.
CC PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
CC PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
CC KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 28
FT TRANSMEM 29 49
FT DOMAIN 50 57
FT TRANSMEM 58 78
FT DOMAIN 79 106
FT TRANSMEM 107 127
FT DOMAIN 128 141
FT TRANSMEM 142 162
FT DOMAIN 163 193
FT TRANSMEM 194 214
FT DOMAIN 215 230
FT TRANSMEM 231 251
FT DOMAIN 252 276
FT TRANSMEM 277 297
FT DOMAIN 298 337
FT DISULFID 96 173
FT CARBOHYD 6 6
FT CARBOHYD 169 169
FT CARBOHYD 180 180
FT CARBOHYD 262 262
SQ SEQUENCE 337 AA; 38541 MW; B9B53940F895F245 CRC64;

Query Match 19.6%; Score 339.5; DB 1; Length 337;
Best Local Similarity 29.8%; Pred. No. 1.1e-14;
Matches 90; Conservative 55; Mismatches 140; Indels 17; Gaps 8;

QY 25 VFPALYTVVFLGTGLTLALWVFWH-IPSSSTFIYKNTLVADLIIMLPFKILSDS 83
DB 25 VYSTLYSMISYVGFENGFLVLYLKTYHKKSAFOVYMINLAVADLCVCTLLPLRVVYV 84

QY 84 HLAPOWLRAPVCRFSVIFETMYGVGLGLAFDRFLKIIRPLNIFLKKPVEAKTVS 143
DB 85 HKGIWLPFGDFLCRLSTYALYVNLCSIFFTAMSEFRCAIIVFPVQNLNLTQKKARFVC 144

QY 144 IFWFFLFIPLNMLISNKEATPSSVKKCASLKGPLGLKWHOM-VNNICQFI-FWTVFI 201
DB 145 VGIWIFVYILTSP-FLMAKPKQDEKNTKCFEPQDQTKNHVLYHVSFLVGFITPFI 203

QY 202 LMLVFIYVIAKKVYSYRSKSKDRKNNKLEGVFVVAVFVCFAPFHARVPYTHSQ 261
DB 204 IIVCYTMI---ILTLKSKMKKNSHKKRAIGIMVNTAAFLVSEMPYHIQRTIHLHFL 260


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OY 262 TNKRTDC----RLQNLFIAKETTLFLAATNICMDPLIYIFLCKRTEKLPOMGRKTTA 317
Db 261 HNETHPCDSVLRMOKSVI-----TLSLAASNCCEFDPLLYFFSGNFRKRLSTF--RKHSL 314
OY 318 SS 319
Db 315 SS 316

RESULT 9
CLUTL_PIG STANDARD; PRT; 340 AA.
ID CLUTL_PIG
AC 095N02;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1).
GN CysLTR1 OR CysLTR1.
OS Sus scrofa (Pig).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OX Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN NCBI_TaxID=9823;
RP [1]
RA SEQUENCE FROM N.A.
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furuichi K.;
RT "Characterization of cloned rat and porcine cysteinyl leukotriene
RT receptors.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Receptor for cysteinyl leukotrienes mediating
CC constriction of the microvascular smooth muscle during an
CC inflammatory response. This response is mediated via a G-protein
CC that activates a phosphatidylinositol-calcium second messenger
CC system (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
CC -----
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AB052686; BAB60826.1;
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PROSITE; PS00237; G-PROTEIN_RECEP_F1_1; FALSE_NEG.
DR PROSITE; PS50262; G-PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT DOMAIN 1 31
FT TRANSMEM 32 52
FT DOMAIN 53 60
FT TRANSMEM 61 81
FT DOMAIN 82 109
FT TRANSMEM 110 130
FT DOMAIN 131 144
FT TRANSMEM 145 165
FT DOMAIN 166 196
FT TRANSMEM 197 217
FT DOMAIN 218 233
FT TRANSMEM 234 254
FT DOMAIN 255 279
FT TRANSMEM 280 300
FT DOMAIN 301 340
FT DISULFID 340 340
FT CARBOHYD 99 176
FT CARBOHYD 6 6
FT CARBOHYD 18 18
FT CARBOHYD 172 172
FT CARBOHYD 265 265
SQ SEQUENCE 340 AA; 38986 MW; 54F9372A121CE413 CRC64;

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Query Match 19.5%; Score 337.5; DB 1; Length 340;
Best Local Similarity 29.4%; Pred. No. 1.4e-14;
Matches 91; Conservative 52; Mismatches 142; Indels 25; Gaps 8;
OY 25 VEPALYTVVFLTGILLNTLALWVFW-IPSSSTFIYLYKNTLVADLIMTLMPFKILSDS 83
Db 28 VSTLYSMITVVGFEFGNGFVLYLYKTYHEKSAYQVYMINLAVADLLCVCTPLRVVYV 87
OY 84 HLAFWOLRAFCVCRSSVIEFETMYGIVLLGLIAFDRFLKIRPLRNIFLKKPVFAKTVS 143
Db 88 HKGIWLFGEDELRLSTYALYVNLVCSIFEMTAMSFRCIAIVFPVQINLITHKKAIVC 147
OY 144 IFIWFLEFISLPNMLSNKEATPSSVKKCASLKGPLGLKWHQWV-NNICOFI-FWTVPI 201
Db 148 IAIWIFVILTSSP-FLMSTSYKDEKNNTKCFEPPOXNOAKYHVLVHVSFVGFITPV 206
OY 202 LMLVFYVIAKKVYDSYRKSCKDRKNNKKLEGVFVVAVFFVCFAPFHARVPYTHSQ 261
Db 207 IIVCYTMI---ILTLKNSMKKNISSRKKAIIGMIIVTAAFLISFMPYHIQRTIHLHL 263
OY 262 TNKRTDC----RLQNLFIAKETTLFLAATNICMDPLIYIFLCKRTEKLPOMGRKTTA 317
Db 264 HNDTKHCDVLRMOKSVXI---TLSLAASNCCEFDPLLYFFSGNFRKRLSTF----- 309
OY 318 SSQENHSSQT 327
Db 310 STFRKHSLSLT 319

RESULT 10
PAFR_HUMAN STANDARD; PRT; 342 AA.
ID PAFR_HUMAN
AC P25105;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Platelet activating factor receptor (PAF-R).
GN PAFR OR PAFR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92028922; PubMed=1656963;
RA Ye R.D., Prossnitz E.R., Zou A., Cochran C.G.;
RT "Characterization of a human cDNA that encodes a functional receptor
RT for platelet activating factor.";
RL Biochem. Biophys. Res. Commun. 180:105-111(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Leukocyte;
RX MEDLINE=92041873; PubMed=1657923;
RA Nakamura M., Honda Z., Izumi T., Sakanaka C., Mutoh H., Minami M.,
RA Bito H., Seyama Y., Matsumoto T., Noma M., Shimizu T.;
RT "Molecular cloning and expression of platelet-activating factor
RT receptor from human leukocytes.";
RL J. Biol. Chem. 266:20400-20405(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92250505; PubMed=1374385;
RA Kunz D., Gerard N.P., Gerard C.;
RT "The human leukocyte platelet-activating factor receptor. cDNA
RT cloning, cell surface expression, and construction of a novel
RT epitope-bearing analog.";
RL J. Biol. Chem. 267:9101-9106(1992).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=92347886; PubMed=1322356;
RA Seyfried C.E., Schweickart V.L., Godiska R., Gray P.W.;
RT "The human platelet-activating factor receptor gene (PAFR) contains
RT no introns and maps to chromosome 1.";
RL Genomics 13:832-834(1992).

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RN [5]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Heart;
 RX MEDLINE-93112021; PubMed-1281995;
 RA Sugimoto T., Tsuchimochi H., McGregor C.G., Mutch H., Shimizu T.,
 RA Kurachi Y.;
 RT "Molecular cloning and characterization of the platelet-activating
 RT factor receptor gene expressed in the human heart.";
 RL Biochem. Biophys. Res. Commun. 189:617-624(1992).
 RN [6]
 RP SEQUENCE FROM N.A.
 RA Behal R.H., Debussere M.S., Olson M.S.;
 RL Submitted (XXX-1992) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-93192035; PubMed-8383507;
 RA Chase P.B., Halonen M., Regan J.W.;
 RT "Cloning of a human platelet-activating factor receptor gene:
 RT evidence for an intron in the 5'-untranslated region.";
 RL Am. J. Respir. Cell Mol. Biol. 8:240-244(1993).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; M80436; AAA60001.1; -
 DR EMBL; M76674; AAA60002.1; -
 DR EMBL; D10202; BAA01050.1; -
 DR EMBL; M88177; AAA60214.1; -
 DR EMBL; S52624; AAB24695.2; -
 DR EMBL; L07334; AAA60108.1; -
 DR EMBL; S56396; AAB25755.1; -
 DR PIR; JH0479; JH0479.
 DR PIR; A40191; A40191.
 DR PIR; A41079; A41079.
 DR GCRDb; GCR_0186; -
 DR GCRDb; GCR_0260; -
 DR GCRDb; GCR_0285; -
 DR GCRDb; GCR_0414; -
 DR GCRDb; GCR_0478; -
 DR GCRDb; GCR_0548; -
 DR GCRDb; GCR_0731; -
 DR MIM; 173393; -
 DR InterPro: IPR000276; GPCR_Rhodpsn.
 DR Pfam: PF00001; 7tm_1; 1.
 DR PRINTS; PRO1153; PAFRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
 KW G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis;
 KW Polymorphism.
 RN DOMAIN 1 16
 FT TRANSSEM 17 38
 FT DOMAIN 39 54
 FT TRANSSEM 55 74
 FT DOMAIN 75 91
 FT TRANSSEM 92 113
 FT DOMAIN 114 133
 FT TRANSSEM 134 155
 FT DOMAIN 156 184
 FT TRANSSEM 185 205
 FT DOMAIN 206 233
 FT TRANSSEM 234 254
 FT EXTRACELLULAR (POTENTIAL).
 FT 1 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 2 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 3 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 4 (POTENTIAL).
 FT EXTRACELLULAR (POTENTIAL).
 FT 5 (POTENTIAL).
 FT CYTOPLASMIC (POTENTIAL).
 FT 6 (POTENTIAL).

FT DOMAIN 255 276
 FT TRANSSEM 277 296
 FT DOMAIN 297 342
 FT DISULFID 90 173
 FT CARBOHYD 169 169
 FT VARIANT 224 224
 FT VARIANT 224 224
 FT VARIANT 338 338
 FT VARIANT 338 338
 FT CONFLICT 28 28
 FT CONFLICT 66 66
 FT CONFLICT 95 95
 FT CONFLICT 227 228
 FT CONFLICT 227 228
 FT CONFLICT 247 247
 FT CONFLICT 316 316
 SQ SEQUENCE 342 AA; 39203 MW; 890073C9EBA79228 CRC64;
 Query Match 19.4%; Score 336.5; DB 1; Length 342;
 Best local similarity 26.2%; Pred. No. 1.6e-14;
 Matches 87; Conservative 75; Mismatches 137; Indels 33; Gaps 9;
 QY 18 DTRIVQVLPALYTVFELTGILNTLALVYFVHIPSSSTF--IYLNKNTLVADLIMTL 74
 DB 10 DSEFRYTLFPYVSIIFVLGVIANGVYLVFARLYPCCKFNEIKIFVNLTMADMLFLIT 69
 QY 75 LPEKILSDSHLAPWQLRAFCVCRSSVFEYETMYGVILGLIAFDRLKIRPLRNIFLK 134
 DB 70 LPLMIVYVQNGNMILPKFLCNVAGCLEFFINTYCSVAFLGVITYNRFQAVTRPIKTAQAN 129
 QY 135 KPVFAKTVSFIWFLEFISLPNMLSKNEATPSS----VKKAS--LKGPLGLKWHQM 187
 DB 130 TRKRGISLSLVIWAIVGASVFLILDSINTVPSAGSGNVTRCFEYHEKGSVPV--LI 186
 QY 188 VNNIQRFITVTFILMLVFYVVIKAYDSYRKSCKDRKNKKLEGR---VEVVAVF 243
 DB 187 IHIFVSEFLEVLILFCNLVITRTL----MQPVQQRNAEYKRALMVCVTLAVF 241
 QY 244 FVCFAPFHPARVPYTHSQTNNKTDCRLQNLFIKETTLLFLAATNIGMDPLIYFLCKKF 303
 DB 242 IICFVPHVYVQLPWLALGFGQ-DSKRFQAINDAHQVTLCLSTNCVLDVIVYCFITKKE 300
 QY 304 ----TEKLEPCMQRKKTASSQENHSQTDNIT 331
 DB 301 RKHLTEKEYSMR-----SSRKCSRAFTDTVT 326
 RESULT 11
 PAFR_CAVPO
 ID PAFR_CAVPO STANDARD; PRT; 342 AA.
 AC P21556;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).
 GN PAFR.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Hystriognathi; Cavidae; Cavia.
 OX NCBI_TaxID-10141;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Lung;
 RX MEDLINE-91101726; PubMed-1846231;
 RA Honda Z.-I., Nakamura M., Miki I., Minami M., Watanabe T., Seyama Y.,
 RA Okado H., Toh H., Ito K., Miyamoto T., Shimizu T.;
 RT "Cloning by functional expression of platelet-activating factor
 RT receptor from guinea-pig lung.";
 RL Nature 349:342-346(1991).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL.

CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 DR EMBL; X56736; CAA40060.1; -
 DR GCRDB; GCR_0034; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01153; PAFRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 38 1 (POTENTIAL).
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 113 3 (POTENTIAL).
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 4 (POTENTIAL).
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL).
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 234 254 6 (POTENTIAL).
 FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 277 296 7 (POTENTIAL).
 FT DOMAIN 297 342 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 173 BY SIMILARITY.
 SQ SEQUENCE 342 AA; 38984 MW; B6413B3A5C87B175 CRC64;

Query Match 19.2%; Score 331.5; DB 1; Length 342;
 Best Local Similarity 27.9%; Pred. No. 3.3e-14;
 Matches 99; Conservative 65; Mismatches 128; Indels 63; Gaps 15;

OY 10 NRSECPDRTRIVOLVLPALYTVFLGILNTLALWVFVHI-PSS-STFIYLYKNTLY 66
 DB 4 NSSSRV--DSEFRYTLFPVIVSYIFVLGIANGYVLMVFARLYPSKLNLIKIFVNLTV 61
 OY 67 ADLIMTLMPFKILSDSHLAPWQLRAFCRSSVIFETMYGVIGVLLGLIAFDRLKIR 126
 DB 62 ADLFLITLPLMIVYISNOGNWFLPKFLCNLAGCLFFINTYCSVAFLGVITVNRQAVKY 121
 OY 127 PLRNIFLKKPVFAKTVSIFIMFEL-----FFISLPNMILSNKEATFSSVKKCAS--LKG 178
 DB 122 PIKTAQATTRKRGIALSLVIVAAASYFLVMDSTNVVSNK-AGSGNITRCFEHYEKG 180
 OY 179 PLGLKHWQVNNICQFI-FWTVFILMLVEYVYIAKKVYDSYRSKSKDRKN---NKKLEG 234
 DB 181 SKPV---LIHICIVLGFIVFLLILFCNLVYIHTLL---KQPVKQQRNAEYRRRALW 232
 OY 235 KVFVVAVAEVFCFARFHFARVPYT-----HSQTNKTKDCRIQNLFAKETTLF 283
 DB 233 MCTVLAVFVIGFVPHHMVQLPWTLAELGMPSSNHQAIND-----AHQVTLIC 280
 OY 284 LAATNICMDPLIYIFLCKF---TEKLPCMQ-----GRKTTASSQF-----NHS 324
 DB 281 LLSTNCVLDPVYICFLTKERKHLSEKLNIMRSSQKSRVTTDTGTETMAPIINHT 335

RESULT 12
 PAFR_RAT

ID PAFR_RAT STANDARD; PRT; 341 AA.
 AC P46002;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Platelet activating factor receptor (PAF-R).
 GN PAFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Spleen;
 RX MEDLINE=94222063; PubMed=8168510;
 RA Bito H., Honda Z., Nakamura M., Shimizu T.;
 RT "Cloning, expression and tissue distribution of rat
 RT platelet-activating-factor-receptor cDNA.";
 RL Eur. J. Biochem. 221:211-218(1994).
 CC -1- FUNCTION: RECEPTOR FOR PLATELET ACTIVATING FACTOR, A CHEMOTACTIC
 CC PHOSPHOLIPID MEDIATOR THAT POSSESSES POTENT INFLAMMATORY, SMOOTH-
 CC MUSCLE CONTRACTILE AND HYPOTENSIVE ACTIVITY. SEEM TO MEDIATE ITS
 CC ACTION VIA A G PROTEIN THAT ACTIVATE A PHOSPHATIDYLINOSITOL-
 CC CALCIUM SECOND MESSENGER SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: PRESENT IN ALMOST ALL ORGANS INCLUDING SPLEEN,
 CC SMALL INTESTINE, KIDNEY, LUNG, LIVER AND BRAIN.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U04740; AAA18422.1; -
 DR GCRDB; GCR_0985; -
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR01153; PAFRECEPTOR.
 DR PROSITE; PS00237; G_PROTEIN_RECIP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECIP_F1_2; 1.
 DR G-protein coupled receptor; Transmembrane; Glycoprotein;
 KW Chemotaxis.
 FT DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 17 38 1 (POTENTIAL).
 FT DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 55 74 2 (POTENTIAL).
 FT DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 92 113 3 (POTENTIAL).
 FT DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 134 155 4 (POTENTIAL).
 FT DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 185 205 5 (POTENTIAL).
 FT DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 234 254 6 (POTENTIAL).
 FT DOMAIN 255 276 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 276 295 7 (POTENTIAL).
 FT DOMAIN 296 341 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 4 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT DISULFID 90 173 BY SIMILARITY.
 SQ SEQUENCE 341 AA; 39204 MW; D0AF7290C3D34A5B CRC64;

Query Match 18.6%; Score 322.5; DB 1; Length 341;
 Best Local Similarity 24.6%; Pred. No. 1.2e-13;
 Matches 83; Conservative 77; Mismatches 147; Indels 31; Gaps 9;

OY 18 DTRIVOLVLPALYTVFLGILNTLALWVFVHI-PSS-STFIYLYKNTLVADLIMTL 74
 DB 10 DSEFRYTLFPVIVSYIFVLGIANGYVLMVFARLYPSKLNLIKIFVNLTVADLFLMT 69

QY 75 LPFKILSDSHAPWOLRAFCVCRFSVFYEETMYGVILLGLINADREFLKIIRPLRNIFLK 134
 11 : : : : : : : : : : : : : : : : : :
 Db 70 LPLMIVYYISNEGDMIVHKFLCNLAGCLFEINTYCSVAELGVIYFNRYQAVAYPIKTAQAT 129
 QY 135 KPVFAKTVSJFIWEFL----FFISLEPMILSNKEATPSSVKRICASLKGPLG--LKWHQ 186
 11 : : : : : : : : : : : : : : : : : :
 Db 130 TRKRGITLSIAIWISIATAASYFLATDSTNVPPKKDGSGNITPCFHEHYEPYSVPILVHI 189
 QY 187 MWNNICQFIETVEFIL-MLVEYVVIAKKYDSYRKSXSDDRNNKKLEGKVENVAAVEFY 245
 : : : : : : : : : : : : : : : : : :
 Db 190 FITSCFELVEFLIEYCMMVIIHTLLTRPV---RQRKRPEVK--RALMWCTVLAVEYI 243
 QY 246 CFAPFHFARVPTYTHSQTNNKTDICRLONQLIAKETTLFLATNYICMDPLIYIFLCCKETE 305
 11 : : : : : : : : : : : : : : : : : :
 Db 244 CFVPHHVVDLPWLIAELGYQTN-FHQAINDAHQITLCLSLTNCVLDPVITYCFLTKEPK 301
 QY 306 KL-----PCMGRKTTASSQENHSSQTDNITL 332
 11 : : : : : : : : : : : : : : : : : :
 Db 302 HLSEKEYISMBSRKCSRATSDTCIEYMPANOTPVLP 339

RESULT	ID	CLT1_RAT	STANDARD;	PRT;	339 AA.
DT	01-MAR-2002	(Rel. 41, Created)			
DT	01-MAR-2002	(Rel. 41, Last sequence update)			
DT	01-MAR-2002	(Rel. 41, Last annotation update)			
DT	Cysteinyl leukotriene receptor 1 (CysLTR1).				
GN	CysLTR1 OR CysLTR1.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID-10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Takasaki J., Kamohara M., Salto T., Matsumoto M., Matsumoto S.,				
RA	Ohishi T., Soga T., Matsushime H., Furuchi K.;				
RT	"Characterization of cloned rat and porcine cysteinyl leukotriene				
RT	receptors.";				
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.				
CC	-1- FUNCTION: Receptor for cysteinyl leukotrienes mediating				
CC	constriction of the microvascular smooth muscle during an				
CC	inflammatory response. This response is mediated via a G-protein				
CC	that activates a phosphatidylinositol-calcium second messenger				
CC	system (By similarity).				
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.				
C	-1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.				
C	-----				
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CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch).				
CC	-----				
DR	EMBL; AB052685; BAB60825.1; .				
DR	InterPro; IPR000276; GPCR_Rhodpsn.				
DR	Pfam; PF00001; 7tm_1; 1.				
DR	PROSITE; PS00237; G-PROTEIN_REC_P1_1; FALSE_NEG.				
DR	PROSITE; PS50262; G-PROTEIN_REC_P1_2; 1.				
KW	G-protein coupled receptor; Transmembrane; Glycoprotein.				
FT	DOMAIN 1 30				
FT	TRANSMEM 31 51				
FT	DOMAIN 52 59				
FT	TRANSMEM 60 80				
FT	DOMAIN 81 108				
FT	TRANSMEM 109 129				
FT	DOMAIN 130 143				
FT	TRANSMEM 144 164				
FT	DOMAIN 165 195				
FT	EXTRACELLULAR (POTENTIAL).				
FT	1 (POTENTIAL).				
FT	CYTOPLASMIC (POTENTIAL).				
FT	2 (POTENTIAL).				
FT	EXTRACELLULAR (POTENTIAL).				
FT	3 (POTENTIAL).				
FT	CYTOPLASMIC (POTENTIAL).				
FT	4 (POTENTIAL).				
FT	EXTRACELLULAR (POTENTIAL).				

FT	TRANSMEM	196	216	5 (POTENTIAL).
FT	DOMAIN	217	232	CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM	233	253	6 (POTENTIAL).
FT	DOMAIN	254	278	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	279	299	7 (POTENTIAL).
FT	DOMAIN	300	339	CYTOPLASMIC (POTENTIAL).
FT	DISULFID	98	175	BY SIMILARITY.
FT	CARBOHYD	6	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	171	171	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	339 AA;	39143 MW;	281B4IDF050DF8EA CRC64;

Query Match	18.5%;	Score 320.5;	DB 1;	Length 339;
Best Local Similarity	27.8%;	Pred. No. 1.6e-13;		
Matches	84;	Conservative	56;	Mismatches 145;
			Indels	17;
			Gaps	7;

QY	25	VFPALYTVELTGILNTLALMWFVH-IPSSSTFIYLKNTLVADLIMTLMPEKILSDS	83
Dd	27	VYSTMSMISVGVGFNGNSFVLVIKTYHEKSASFQVTYMINLAIDLCTEPLERVVVYV	86
QY	84	HIAWQLRAFCVRFSSEVFYEETMYVGIVLLGLIAEDRFKLIRPLRNIFLKREFAKTVS	143
Dd	87	HKGMFEFGDFLCRLTTYALYVNLYCSIFEWTAMSFRCVAIVEPVONINLYOKKAREVC	146
QY	144	IFIWEFLFISLPNMILSNKEATPSSVKKCASLKGPLGLKWOMVNNNICOFIEWTV--FI	201
Dd	147	VGIWIEFVILTSP-FLLSKSYODEKNNTKCEEPPODKQTKKYVLVLHYVSLIEGPIIIPV	205
QY	202	IMLYEVYVIAKKVYDSYRKSCKDRKNKKLEGKVYVVAVVEFVCFAPFHFAVPYTHSQ	261
Dd	206	TIIVCYTM-----ILTLLKNTMKKNLPSRRKAIGMIIVTTAAFLVSEMPYHIORAIHLHL	262
QY	262	TNNKTDG----RLQNOLFIAKETLELATNICYMDPLIYIFLCKKFTEKLEPCMOGRKTTA	317
Dd	263	HSETRSCDSDLRMOKSVI---TLSLASNCCEFDPLLYFFSGGNERRRLSTF--RKHS	316
QY	318	SS 319	
Dd	317	SS 318	

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RESULT 14
ID CLT1_MOUSE STANDARD; PRT; 352 AA.
AC Q99JA4; Q9JKA7; Q9JL71;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Cysteinyl leukotriene receptor 1 (CysLTR1) (Cysteinyl leukotriene D4
GN receptor) (LTD4 receptor).
OS CysLTR1 OR CysLTR1 OR CysLTR1R.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC STRAIN=129SV;
RX PubMed=11226226;
RA Maekawa A., Kanaoka Y., Lam B.K., Austen K.F.;
RT "Identification in mice of two isoforms of the cysteinyl leukotriene 1
RT receptor that result from alternative splicing.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:2256-2261(2001).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC STRAIN=C57BL/6; TISSUE=Trachea;
RX PubMed=11705452;
RA Martin V., Sawyer N., Stocco R., Unett D., Lerner M.R., Abramovitz M.,
RA Funk C.D.;
RT "Molecular cloning and functional characterization of murine
RT cysteinyl-leukotriene 1 (CysLT1) receptors.";
RL Biochem. Pharmacol. 62:1193-1200(2001).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 1).

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DR	EMBL; D50872; BAA09468.1; -.
DR	GCRDb; GCR_1618; -.
DR	MGI; MGI:106066; Ptafr.
DR	InterPro; IPR000276; GPCR_Rhodpsn.
DR	Pfam; PF00001; 7tm_1; 1.
DR	PRINTS; PRO1153; PAFRECEPTOR.
DR	PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR	PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW	G-protein coupled receptor; Transmembrane; Glycoprotein; Chemotaxis.
KW	
FT	DOMAIN 1 16 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 17 38 1 (POTENTIAL).
FT	DOMAIN 39 54 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 55 74 2 (POTENTIAL).
FT	DOMAIN 75 91 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 92 113 3 (POTENTIAL).
FT	DOMAIN 114 133 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 134 155 4 (POTENTIAL).
FT	DOMAIN 156 184 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 185 205 5 (POTENTIAL).
FT	DOMAIN 206 233 CYTOPLASMIC (POTENTIAL).
FT	TRANSMEM 234 254 6 (POTENTIAL).
FT	DOMAIN 255 275 EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM 276 295 7 (POTENTIAL).
FT	DOMAIN 296 341 CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD 4 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD 169 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	DISULFID 90 BY SIMILARITY.
SEQUENCE	341 AA; 39148 MW; CA8CDBDB8D26897 CRC64;

Query Match	18.28;	Score 315.5;	DB 1;	Length 341;
Best Local Similarity	25.48;	Pred. NO. 3.2e-13;		
Matches 86;	Conservative 77;	Mismatches 144;	Indels 31;	Gaps 11;

[illegible]

Search completed: October 11, 2002, 14:49:06
Job time : 14 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:47:34 ; Search time 23 Seconds
(without alignments)
1391.206 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731
Sequence: 1 MNTVMQGFNRSERCPDRTR.....KTTASSQENHSSQTDNITLG 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_71:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	365	21.1	361	2	B45680
2	336.5	19.4	342	2	A40191
3	331.5	19.2	342	2	S13638
4	322.5	18.6	341	2	S43252
5	315.5	18.2	341	2	S63666
6	309.5	17.9	359	2	S15403
7	305.5	17.6	359	2	A48857
8	300.5	17.4	359	2	JC1104
9	300	17.3	362	2	S33733
10	300	17.3	373	2	JE0087
11	299	17.3	359	2	JH0621
12	298.5	17.2	420	2	I51667
13	298	17.2	359	2	S44425
14	297	17.2	359	2	JC2134
15	296.5	17.1	308	2	I50241
16	292.5	16.9	365	2	S68679
17	292	16.9	370	2	JC5549
18	292	16.9	392	2	S65693
19	292	16.9	400	2	I56553
20	291	16.8	398	2	I56517
21	290.5	16.8	359	2	A42656
22	290.5	16.8	359	2	I39418
23	289.5	16.7	358	2	A53752
24	286	16.5	359	2	JC1194
25	286	16.5	398	2	A57510
26	285.5	16.5	359	2	JQ1516
27	285	16.4	380	2	A55259
28	284	16.4	373	2	JC4737
29	284	16.4	380	2	JC2338

30	283.5	16.4	344	2	T09508	Intron 17 purinerg
31	283.5	16.4	360	2	G02064	G protein-coupled
32	283.5	16.4	380	2	I38435	angiotensin recept
33	283	16.3	362	2	A39714	G protein-coupled
34	283	16.3	380	2	A48227	kappa opioid recep
35	282	16.3	380	2	S36143	kappa opioid recep
36	282	16.3	398	2	I56504	mu opioid receptor
37	279.5	16.1	363	2	I57940	somatostatin recep
38	279.5	16.1	373	2	JC4162	P2Y receptor - bov
39	279	16.1	391	2	A41795	somatostatin recep
40	279	16.1	391	2	C41795	somatostatin recep
41	279	16.1	391	2	A39297	interleukin-8 rece
42	275.5	15.9	356	2	S42096	protease activat
43	274	15.8	399	2	I48705	interleukin-8 rece
44	272.5	15.7	360	2	A53611	kappa opioid recep
45	272	15.7	380	2	JC2434	

ALIGNMENTS

RESULT 1
B45680
G protein-coupled peptide receptor EBI 2 - human
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_rev18-Nov-1994 #text_change 21-Jul-2000
C/Accession: B45680
R/Birkenbach, M.; Josefsen, K.; Yalamanchili, R.; Ienolr, G.; Kieff, E.
J. Virol. 67, 2209-2220, 1993
A/Title: Epstein-Barr virus-induced genes: first lymphocyte-specific G protein-couple
A/Reference number: A45680; MUID:93188173
A/Accession: B45680
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-361 <BIR>
A/Cross-references: GB:L08177; NID:q292056; PIDN:AAA35924.1; PID:q292057
A/Experimental source: B-lymphocytes
A/Note: sequence extracted from NCBI backbone (NCBIN:127096, NCBIPI:127097)
C/Superfamily: ATP receptor P2u
C/Keywords: G protein-coupled receptor; transmembrane protein

Query Match	21.1%;	Score 365;	DB 2;	Length 361;
Best Local Similarity	27.2%;	Pred. No. 3.9e-24;		
Matches	88;	Conservative	78;	Mismatches 135; Indels 22; Gaps 7;
OY	23	QLEVPALYTVFELTGILNTALMVFVH---	IPSSSTFIYLNKTLVADLIMTLMPFK	78
Db	31	RIVMPLHYSLVFLIGLVGNLALVIVONRKINST---	LYSTNLVISDILFTALPTR	87
OY	79	ILSDSHLAPWQLRAVFCRSSVIFETMYGVLLGLAFDRFLKIIRPLRNIFLKPVF	138	
Db	88	IAYYAMGFDMRIGDALCRITALVFYINTYAGVNFMTCLSDRFIAVVPRLRYNKRRIEH	147	
OY	139	AKTVSIFIFWFLFFISLPNMT--LSNKEATPSSVKKCASLKGPLGLKWHOMVNNICQFIF	196	
Db	148	AKGVCIFFWILVFAQTLPLINPMSKQEAERITCMEYFNFEETKSLPW--ILGACFIGY	205	
OY	197	WTVFIMLVFYVVIKAYDSYRKSRSKDRKN--NKKLEGKVFVVAVFVCFAPFHFARV	255	
Db	206	VLPILITLICYSQICKLEPRAKONPLTEKSGVNNKALNTIILIVFVLCTFYHVAIT	265	
OY	256	PYTHSQT--NNKTDCLRNQQLFIARETTLLFAATFNICMDPLIYIFLCKKFTKLPQMGGR	313	
Db	266	QHMIKKLRFNSFLFECQSQRHSFQISLHFTVCLMNFNCMDPFIYFACKGKYKRYRMMLKR	325	
OY	314	KTTAS-----SQENHSSQTD	328	
Db	326	QVSVSISSAVKSAPEENSRMTE	348	
RESULT 2				
A40191				
platelet-activating factor receptor - human				

C:Species: Homo sapiens (man)
C:Date: 28-Aug-1992 #sequence_revision 28-Aug-1992 #text_change 20-Jun-2000
C:Accession: A40191; JH0479; A41079; JCI359; A42831; I51923
R:Kunz, D.; Gerard, N.P.; Gerard, C.
J. Biol. Chem. 267, 9101-9106, 1992
A:Title: The human leukocyte platelet-activating factor receptor. cDNA cloning, cell surface expression, and functional characterization
A:Reference number: A40191; MUID:92250505
A:Accession: A40191
A:Molecule type: mRNA
A:Residues: 1-342 <KUN>
A:Cross-references: GB:M76674; NID:g456293; PIDN:AAA60002.1; PID:g456294
R:Ye, R.D.; Prossnitz, E.R.; Zou, A.; Cochrane, C.G.
Biochem. Biophys. Res. Commun. 180, 105-111, 1991
A:Title: Characterization of a human cDNA that encodes a functional receptor for platelet-activating factor
A:Reference number: JH0479; MUID:92028922
A:Accession: JH0479
A:Molecule type: mRNA
A:Residues: 1-342 <YER>
A:Cross-references: GB:M80436; NID:g189537; PIDN:AAA60001.1; PID:g189538
R:Experimental source: granulocyte, cell line HL-60
R:Nakamura, M.; Honda, Z.; Izumi, T.; Sakakaka, C.; Mutoh, H.; Minami, M.; Bito, H.; Seyi, J. Biol. Chem. 266, 20400-20405, 1991
A:Title: Molecular cloning and expression of platelet-activating factor receptor from human platelets
A:Reference number: A41079; MUID:92041873
A:Accession: A41079
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-342 <NAK>
A:Cross-references: GB:D10202; GB:D90433; NID:g219975; PIDN:BAA01050.1; PID:g219976
R:Sugimoto, T.; Tsuchimochi, H.; McGregor, C.G.A.; Mutoh, H.; Shimizu, T.; Kurachi, Y.
Biochem. Biophys. Res. Commun. 189, 617-624, 1992
A:Title: Molecular cloning and characterization of the platelet-activating factor receptor from human platelets
A:Reference number: JCI359; MUID:93112021
A:Accession: JCI359
A:Molecule type: mRNA
A:Residues: 1-315, 'N', 317-342 <SUG>
A:Experimental source: heart
A:Note: the authors translated the codon AAT for residue 316 as Lys
R:Seifried, C.E.; Schweickart, V.L.; Godiska, R.; Gray, P.W.
Genomics 13, 832-834, 1992
A:Title: The human platelet-activating factor receptor gene (PTAFR) contains no introns
A:Reference number: A42831; MUID:92347886
A:Accession: A42831
A:Molecule type: DNA
A:Residues: 1-226, 'TG', 229-342 <SEX>
A:Cross-references: GB:M88177; NID:g190697; PIDN:AAA60214.1; PID:g190698
A:Note: sequence extracted from NCBI backbone (NCBIN:109813, NCBIP:109814)
R:Chase, P.B.; Halonen, M.; Regan, J.W.
J. Resplr. Cell Mol. Biol. 8, 240-244, 1993
A:Title: Cloning of a human platelet-activating factor receptor gene: evidence for an intron
A:Reference number: I51923; MUID:93192035
A:Accession: I51923
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-342 <RES>
A:Cross-references: GB:S56396; NID:g298580; PIDN:AAB25755.1; PID:g298581
C:Genetics:
A:Gene: GDB:PTAFR
A:Cross-references: GDB:128806; OMIM:173393
A:Map position: 1p35-1p34.3
C:Superfamily: ATP receptor P2u
C:Keywords: G protein-coupled receptor; transmembrane protein
F:17-38/Domain: transmembrane #status predicted <TRI>
F:54-75/Domain: transmembrane #status predicted <TII>
F:92-113/Domain: transmembrane #status predicted <III>
F:134-155/Domain: transmembrane #status predicted <TIV>
F:184-205/Domain: transmembrane #status predicted <TRV>
F:233-253/Domain: transmembrane #status predicted <TVI>
F:277-297/Domain: transmembrane #status predicted <VII>

[illegible]

RESULT 3

platelet-activating factor receptor - guinea pig
C/Species: Cavia porcellus (guinea pig)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 08-Oct-1999
C/Accession: S13638
R/Honda, Z.; Nakamura, M.; Miki, I.; Minami, M.; Watanabe, T.; Seyama, Y.; Okado, H.;
Nature 349, 342-346, 1991
A/Title: Cloning by functional expression of platelet-activating factor receptor from
A/Reference number: S13638; MUID:91101726
A/Accession: S13638
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-342 <HON>
A/Cross-references: GB:X56736; MID:g49442; PIDN:CAA40060.1; PID:g49443
A/Note: the species of guinea pig is not identified, in GenBank entry CCPAFREC, relea
C/Superfamily: ATP receptor p2u

Query Match	19.28;	Score 331.5;	DB 2;	Length 342;
Best Local Similarity	27.98;	pred. No. 3e-21;		
Matches 99;	Conservative 65;	Mismatches 128;	Indels 63;	Gaps 15;
QY 10	NRSECRPDRTRIVQLVPEADYTVFELTGILNTLALWFWHI--SS--STFIYLKNTLV 66			
DB 4	NSSSRV--DSEFRYTLFPYYSIIFVLGIANGYVLWFAFLYPSSKLEIKIFMVNLTV 61			
QY 67	ADLIMTLMPKILSDSHLAPWQLRAFCRSSVIFETMYGVILLGLIAFDRLKIR 126			
DB 62	ADLFLITLPLMWVYYSNOGNWFLPKFLCNLAGCLFINTYCSVAFLGVITYNRFQAVKY 121			
QY 127	PLRNIFLKKPVEAKTVSIFWFFL-----FFISLPMILSNKEATPSSVKKCAS--LKG 178			
DB 122	PIKTAQATRRKRGIALSLVIVAIVAASFYLWMDSTNVSNK--AGSGNITRCFEHYEKG 180			
QY 179	PLGLKWHQMVNNICOF--FWTVFILMLVFYVVIAKKVDYSYRKS SKDRKN--NKKLEG 234			
DB 181	SKPV----LIHICIVLGFIVFELLILFCNLVITHLL----RQPVKQQRNAEVRRLALW 232			
QY 235	KVEVVAAVEFCFAPEHFARVPYT-----HSQTNKTKDCRLQNLFIAKETILF 283			
DB 233	MVCTVLAVEFICFVPHHMVQLPWTLAELGMPSSNHOAIND-----AHQVTLIC 280			
QY 284	LAATNICMDPLIYIFLCKKF---TEKLPCMQ-----GRKTTASSOE---NHS 324			
DB 281	LLSTNCVLDPAVYCFLTKKFRKHLSEKLNIMRSSQRCRSVTTDTGTEMAIPINH 335			


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A:Reference number: A48857; MUID:932336091
A:Accession: A48857
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-359 <BUR>
A:Cross-references: GB:S59041; NID:g299614; PIDN:AAB:6239.1; PID:g299615
A:Experimental source: proximal tubule cells
A:Note: sequence extracted from NCBI backbone (NCBIN:129600, NCBI:P:129601)
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match      17.6%; Score 305.5; DB 2; Length 359;
Best Local Similarity 26.3%; Pred. No. 5.6e-19;
Matches 93; Conservative 72; Mismatches 157; Indels 31; Gaps 11;

OY 1 MNTTWOGFNR-SERCPDR--IVOLVFPALYVFLTGILINTLA-LWVFVHIPSSST 56
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 3 LNSSTEDGIKRIQDDCPKAGHNYIFWMPTLYSIFVVGIFGNSLAVIVIFYMKLKV 62

OY 57 FLIYKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRSSVIFYETMYGVILGLI 116
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 63 ASVFLNLALADLCFLFLPLMAVYTAMEYRWPFNGNYLCKIASASVSFNLYASVFLTCL 122

OY 117 AFDRLKIIRPLRNIEFLKRVFAKTVSIFIFWFFLEFISLPMJLSNK---EATPSSVKKC 173
   ||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 123 SIDRYLAIVHPMKSRLRRIMLVAKVTCIITIMLAGLASLPAIIRHNVFIENT--NITVC 180

OY 174 A-----SLKGPLGLKHWQNNNICOFIFWTVFILMLVFFVYVIAKKVYDSYRKSCKDRK 227
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 181 AFHYESONSTLPGL--GLTKNIGFLF--PELLITSYTLIWKALKKAYEIQKNPR- 234

OY 228 NNKLEGVVVVAVFVCFAPFHFARVPYTHSQTNKNTDCRIQNLFIAKETTLFLAAT 287
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 -NDIFKIIMATVLEFFFSWVPHQIFTFDLVLIQLGVTHDCRIADIVDTAMPITICLAYF 293

OY 288 NICMDPLIYIFLCKKTEK-LPCMOGRKTTASSQENHSSQ-----TDNIT 331
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 294 NNCNLPLFYGLGKREKXYFLQLLKYIPPKAKSHSNLSTKMSLTSYRPSDNVS 346

RESULT 8
JC1104
angiotensin II receptor type 1 - human
N:Alternate names: angiotensin II receptor 1A
C:Species: Homo sapiens (man)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 21-Jul-2000
C:Accession: JC1104; JQ1402; JH0574; JH0267; A44014; S18983
R:Maury, C.A.; Hwang, O.; Egloff, A.M.; Wu, L.H.; Chung, F.Z.
ochem. Biophys. Res. Commun. 186, 277-284, 1992
Title: Cloning, expression, and characterization of a gene encoding the human angioten
..Reference number: JC1104; MUID:92337608
A:Accession: JC1104
A:Molecule type: DNA
A:Residues: 1-359 <MAU>
R:Furuta, H.; Guo, D.F.; Inagami, T.
Biochem. Biophys. Res. Commun. 183, 8-13, 1992
A:Title: Molecular cloning and sequencing of the gene encoding human angiotensin II type
A:Reference number: JQ1402; MUID:92181475
A:Accession: JQ1402
A:Molecule type: DNA
A:Residues: 1-359 <FOR>
A:Cross-references: EMBL:Z11162; NID:g28709; PID:g28710
A:Experimental source: lymphocyte
R:Bergsma, D.J.; Ellis, C.; Kumar, C.; Nuthulaganti, P.; Kersten, H.; Elshourbagy, N.; G
Biochem. Biophys. Res. Commun. 183, 989-995, 1992
A:Title: Cloning and characterization of a human angiotensin II type 1 receptor.
A:Reference number: JH0574; MUID:92231907
A:Accession: JH0574
A:Molecule type: mRNA
A:Residues: 1-359 <BER>
A:Cross-references: GB:M87290; NID:g178682; PIDN:AAA35535.1; PID:g178683
A:Experimental source: liver
R:Takayanagi, R.; Ohnaka, K.; Sakai, Y.; Nakao, R.; Yanase, T.; Hajl, M.; Inagami, T.; H

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Biochem. Biophys. Res. Commun. 183, 910-916, 1992
A:/Title: Molecular cloning, sequence analysis and expression of a cDNA encoding human
A:/Reference number: JH0267; MUID:92198490
A:/Accession: JH0267
A:/Molecule type: mRNA
A:/Residues: 1-359 <TAK>
A:/Experimental source: liver
R:/Curnow, K.M.; Pascoe, L.; White, P.C.
Mol. Endocrinol. 6, 1113-1118, 1992
A:/Title: Genetic analysis of the human type-1 angiotensin II receptor.
A:/Reference number: A44014; MUID:92375105
A:/Accession: A44014
A:/Status: preliminary
A:/Molecule type: mRNA
A:/Residues: 1-359 <CUR>
A:/Cross-references: GB:M93394; NID:g178680; PID:g178681
A:/Note: sequence extracted from NCBI backbone (NCBIN:111831, NCBIP:111833)
C:/Genetics:
A:/Gene: GDB:AGTRL
A:/Cross-references: GDB:132359; OMIM:106165
A:/Map position: 3q21-3q25
C:/Superfamily: vertebrate rhodopsin
C:/Keywords: G:protein-coupled receptor; glycoprotein; hormone receptor; transmembrane
F:/30-53/Domain: transmembrane #status predicted <TM1>
F:/65-90/Domain: transmembrane #status predicted <TM2>
F:/103-124/Domain: transmembrane #status predicted <TM3>
F:/145-167/Domain: transmembrane #status predicted <TM4>
F:/194-216/Domain: transmembrane #status predicted <TM5>
F:/241-264/Domain: transmembrane #status predicted <TM6>
F:/281-305/Domain: transmembrane #status predicted <TM7>
F:/4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match      17.4%; Score 300.5; DB 2; Length 359;
Best Local Similarity 25.9%; Pred. No. 1.5e-18;
Matches 92; Conservative 71; Mismatches 157; Indels 35; Gaps 11;

QY   1 MNTVMOGFNR-SERCPDRTR--IVQLVFPALYTVEFLGILLNTL-ALWVFVHIPSSST 56
      ::::| | | | | : : : | | : : : | | : : : |
Db    3 LNSSTEDGIKRIQDDCPKAGRNHYIFWMIPTLYSIIEVGIFGNSLVIVIFYMKLTQV 62
      ::||| ||| | | : : : | | : : : | | : : : |
QY   57 FIYVKNTLVADLIMTLMPEKILSDSHLAPWOLRAFCRFSSVIETMYGVIGLLGLI 116
      ::||| ||| | | : : : | | : : : | | : : : |
Db    63 ASVELLNALADLCFLTLPLMAVYTAMEYRWPFEGNYLCRTASASVSFNLYASVELLTCL 122
      ::||| ||| | | : : : | | : : : | | : : : |
QY   117 AFDFRLKIIRPLRNIFLKRPFAKTVSIFIFEFFELSLPMWLSNK---EATPSSVKKC 173
      : ||:| | : : : | | : : : | | | | | | | : : : |
Db    123 SIDRYLAIVHPMKSRLRRITMLAKVTCTIIWLLAGLASLPAILHRNVFEIENT--NITVC 180
      : ||:| | : : : | | : : : | | | | | | | : : : |
QY   174 A-----SLKGPLGLKWHQVNNICOFIFWTVFILMLVFYVIAKKVDSYRSKSKDKRK 227
      -| | | | | : : : | | : : : | | : : : | | : : : |
Db    181 AFHYESQNSTLPIGL---GLTKNILGFLE--PELLILTSYTLIWALKKAYEIQKNKPR- 234
      -| | | | | : : : | | : : : | | : : : | | : : : |
QY   228 NNKKEGVVVVAVFECFAPFHFAVPYTHSQTNKTDCLRLOQLFIACKETTLFLAAT 287
      | | | | | : : : | | : : : | | | | | | | : : : |
Db    235 -NDIDFKIIMAIVLFFESWIPIHQIFTFDLVDLIQLGITRDCRIADIVDTPAMPITICIAVF 293
      | | | | | : : : | | : : : | | | | | | | : : : |
QY   288 NICMDPLIYIFLCKKFTFKLPCMGRKTTASSQENHS-----QTONT 331
      | | | | | | | | | : : : | | : : : | | : : : |
Db    294 NNCINPLFYFGFGKKF--KRYFLQLLKYIPPKAKSHSNLSTKMSTLSYRPSDNVS 346
      | | | | | | | | | : : : | | : : : | | : : : |

RESULT 9
S333733
G protein-coupled receptor - chicken
C/Species: Gallus gallus (chicken)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-Sep-1999
C/Accession: S333733
R/Webb, T.E.; Simon, J.; Krishek, B.J.; Bateson, A.N.; Smart, T.G.; King, B.F.; Burns
FEBS Lett. 324, 219-225, 1993
A>Title: Cloning and functional expression of a brain G-protein-coupled ATP receptor.
A/Reference number: S333733; MUID:93285340
A/Accession: S333733
A>Status: preliminary

```

A;Molecule type: mRNA
A;Residues: 1-362 <WEB>
A;Cross-references: EMBL:X73268; NID:g3395084; PIDN:CAA51716.1; PID:g3395085
C;Superfamily: ATP receptor P2u
C;Keywords: G protein-coupled receptor; transmembrane protein

Query Match	17.38;	Score 300;	DB 2;	Length 362;
Best Local Similarity	26.18;	Pred. No. 1.7e-18;		
Matches	87;	Conservative	69;	Mismatches 157;
			Indels	20;
			Gaps	9;

```
QY      10 NRSECRPROTRIVOLVF-PALTYVVEFLGILLNTLALMVEV-HIPSSSTFIYLKNTLVA 67
        | : : | | : : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      26 NATTKCSLTGTGFQFYLLPVIYILVITGTGLNSVAIMWFHFHMRPMGISIYMENLALA 85
QY      68 DLIETMLLPFKILSDSHLAPMOIRAFVCRESSVIFETYMYGVILLGLIAEDRELKIIRP 127
        | : | | | | : : : | : : | : : | : : | : : | : : | : : | : : |
Db      86 DELYVLTLPALIEYYFNKTWDWFGDMCKLRORFIFHVNLXGSIPLFCISVHRYTGVHP 145
QY      128 LRNIFLKRPVEAKTVSIFEFLEFISLPNMILSNKEATPSSVKRCASLKGPLGLKWHQM 187
        | : : : | | | : : : : | : : | : : | : : | : : | : : | : : |
D       146 LKSLGRKKKNNAVYVSSLVMALVAVAIPILEYSGTGVRRNKTIITCYDTTADEYLRSY-F 204
QY      188 VNNICQ--FIFMTVEFILMEVEYVIAKK-VYDSYRKSXSODRKNN--KLEGKVFWVA 241
        | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      205 VYSMCTVTVMFCIPFIVILGCYGLIVAKALIY-----KDLDNSPLRKRKSIIYLVILT 256
QY      242 VEVVCFAPFHFARVPYTHSQTNKTD--CRLQNOLFIAKETTLFLAATNICMDPLIYIFL 299
        || | : | : | : : : : | : : : : | : : : : | : : : : | : : : : |
Db      257 VFAVSYPFHVMKTLNLRARDFOCPOMCAFNDKVYATYQVTRGLASLNSCVDPILYFLA 316
QY      300 CKKFTEKLPCMGRKRTASSOENHSSOTDNITL 332
        | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db      317 GDTFRRL-SRATRKSRSRSEPNOVOSKSEEMTL 348
```

```

RESULT 10
JE0087
delta opioid receptor - zebrafish
C:Species: Danio rerio
C:Date: 14-May-1998 #sequence_revision 29-May-1998 #text_change 20-Jun-2000
C:Accession: JE0087
R:Barriallo, A.; Gonzalez-Sarmiento, R.; Porterous, A.; Garcia-Isidoro, M.; Rodriguez, R.
Biochem. Biophys. Res. Commun. 245, 544-548, 1998
A:Title: Cloning, molecular characterization, and distribution of a gene homologous to delta
A:Reference number: JE0087, MUID:98238678
A:Accession: JE0087
A:Molecule type: mRNA
A:Residues: 1-373 <BAR>
A:Cross-references: EMBL:AJ001596; NID:g2739230; PIDN:CA04862.1; PID:g2739231
C:Comment: This protein mediates the effects of morphine and the related drugs, and is th
C:Superfamily: vertebrate rhodopsin
C:Keywords: glycoprotein
F:21,37/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match	17.3%;	Score 300;	DB 2;	Length 373;
Best Local Similarity	29.08;	Pred. No. 1.7e-18;		
Matches	89;	Conservative	55;	Mismatches 145;
				Indels 18;
				Gaps 9;

QY	5	VMQGFNRSECRPDTR--IVQLVFPALVTVEFLTGLLNTLALWFEVHIPSSTFEI-ITYL	61
		: : : : : : : : :	
Db	32	VPDGRNTEPNPVKSRIIAISITALYSVICVGLGNILVMYGVARRYTKLKATANIYI	91
		: : : : : : : : :	
QY	62	KNTLVADLIMTLMPEKILSDSLA-EPQLRAFCRESSVIFYETMWYGIYLLGLIAFDR	120
		: : : : : : : : : : : :	
Db	92	FNLLADALATSTLPFQ--STKYLMTWPEGELLCKVIAIDYYNMFISFTLTMSVDR	149
		: : : : : : : : : : : :	
QY	121	FLKIIRPLRNIFLKKPVFAKTVSIFIMEFLEFISLPNMILSNKEATPSSVYKCKASLGP	180
		: : : : : : : : : : : : : :	
Db	150	YIAVCHVRALEERTPIKAKIINVCIMILSSAVGVPIMIMAVTRVTINONTTVC-MLKFPD	208
		: : : : : : : : : : : : :	
QY	181	GLKMHQWVNNICQFIF-WTVFILMLVF---YVVIACKVYDSYRKSCKDRKNKKLEGV	236
		: : : : : : : : : : : : :	
Db	209	PDWYMDTVTKICVFIFAFVVPVLVITCYGIMILRLKSVRLSGSKIEKDR-NMRRITRMV	267
		: : : : : : : : : : : :	

QY 237 FVVVAVEFCEAFEHFARVPYTHSGTNKCTDCLQNQLFAKETTLFLAATNICMDPLIY 296
||| : : : : : || : : : : :
Db 268 LVVVAAFICWTPIHIFIEKTLVDINOK-----NPFVATSWHLHRTGYTNSSLNAPVLY 321
||| : : : : : || : : : : :

QY	297	IFLCKKF	303
		:	
Db	322	AFIDENF	328

RESULT 11
JH0621
angiotensin II receptor 1A - mouse
C:Species: Mus musculus (house mouse)
C:Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 24-Nov-1999
C:Accession: JH0621; JCl193
R: Sasamura, H.; Hein, L.; Krieger, J.E.; Pratt, R.E.; Koblika, B.K.; Dzau, V.J.
Biochem. Biophys. Res. Commun. 185, 253-259, 1992
A:Title: Cloning, characterization, and expression of two angiotensin receptor (AT-1)
A:Reference number: JH0621; MUID:92287102
A:Accession: JH0621
A:Molecule type: DNA
A:Residues: 1-359 <SB>
A:Cross-references: GB:S37484; NID:g249945; PIDN:AAB22269.1; PID:g249946
A:Experimental source: straln Balb/c
R: Yoshida, H.; Kakuchi, J.; Guo, D.F.; Furuta, H.; Iwai, N.; van der Meer-de Jong, R.
Biochem. Biophys. Res. Commun. 186, 1042-1049, 1992
A:Title: Analysis of the evolution of angiotensin II type 1 receptor gene in mammals
A:Reference number: JCl193; MUID:92359981
A:Accession: JCl193
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-6, 'I', '8-19, 'IS', '22-37, 'M', '39-133, 'K', '135-359 <YOS>
C:Superfamily: vertebrate rhodopsin
C:Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane p
F:37-57/Domain: transmembrane #status predicted <TM1>
F:65-85/Domain: transmembrane #status predicted <TM2>
F:103-123/Domain: transmembrane #status predicted <TM3>
F:145-165/Domain: transmembrane #status predicted <TM4>
F:201-220/Domain: transmembrane #status predicted <TM5>
F:241-261/Domain: transmembrane #status predicted <TM6>
F:286-306/Domain: transmembrane #status predicted <TM7>
F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted
F:331,338/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match	17.38;	Score 299;	DB 2;	Length 359;
Best Local Similarity	26.98;	Pred. No. 2e-18;		
Matches 91;	Conservative 66;	Mismatches 157;	Indels 24;	Gaps 10;

```

QY 1 MNTVMOGFNR-SERCPDRR--IVQVLPALYTVVFLGILLNTL-ALWFEVHIPSSST 56
   : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : |
Db 3 LNSSTEDGIKRIQDDCPRGRHSYIFVMIPLTYSITFEVVGIFGNSLVIVITVYFMKLTv 62

QY 57 FIYYKNTLVADLIMTLMPEKILSDSHLAPWQLRAFCVCRESSVIFYETMYGIVLGLI 116
   : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 63 ASVFLNLALADLCFLTLPLMAVYTAMEYRWPFGNHCLKIASASVSFNLYASVELLTCL 122

QY 117 AEDRELKTIIRPLRNIFLKRVEAKTVSIFIFWELFETSLPNMILSNK--EATPPSVKKC 173
   : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 123 SIDRYLAIVHPMKSRLRRMLVAKVTCIIIMLAGLASLPVHIRNVFIENT--NITVC 180

QY 174 A-----SLKGPLGLKWHQWVNNICQFIWFVFIMLVEVYVIAKKVYDSYRKS SKDRK 227
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 181 AFHYESRNSTPIGL--GLTKNIGFLF--PFLILTSYTLIMWALKKRAYEIQKNKPR- 234

QY 228 NNKKLEGKVFVVAVFAFCFAPFHFARVPYTHSQTNNKTDICRLQNLFIARETTLFLAAT 287
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 235 -NDDIFRIIMAIVLFFFFSWVPHOIFTEFLDVLIDLGVIHDCKIADIYDTAMPITICIAF 293

QY 288 NICMDPLIYIFLCKKFTYKLPCCMOGRKTTASSQENHSS 325
   | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 294 NNCINPLFYGFLGKF--KKYFLQLLKYIPPRKSHSS 329

```


RESULT 12

151667

Thrombin receptor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000

C:Accession: 151667

R:Gerszten, R.E.; Chen, J.; Ishii, M.; Ishii, K.; Nanevich, T.; Turck, C.W.; Vu, T.H.; Nature 368, 648-651, 1994

A:Title: Thrombin receptor's specificity for agonist peptide is determined by its extrac

A:Reference number: 151667; MUID:94195429

A:Accession: 151667

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-420 <GER>

A:Cross-references: EMBL:U09632; NID:9495197; PIDN:AAA18498.1; PID:9495198

Query Match

17.2%; Score 298.5; DB 2; Length 420;

Best Local Similarity 26.5%; Pred. No. 2.6e-18;

Matches 86; Conservative 61; Mismatches 131; Indels 47; Gaps 12;

OY 27 PALYTVVLTGILNLTALMVF-----VHIPSSSTFIYLNKNTLVADLIMTLMPFKILS 81

DB 105 PSLYTVVFIYGLPLNLAIIFLEFKMKVRKPA-----VYMLNLAIADVFVSVLPFKIA- 159

OY 82 DSHLA--PWOLRAVCRSSVIFETMYGVILGLIAPDRFLKIIRPLRNLFLKPPVEA 139

DB 160 -YHLSGNDWLFPGMKRIVTAIFYCMYCSVLIAISYDRFLAVVYPMHSLSWRTMSRA 218

OY 140 KTVSIFWFFLEFISLPMILSNKEATPS-SYKCAASLKGPLGK--WHQVNNICQFIF 196

DB 219 YMACSFIMLISASTIPLLVTEQTKIPRLDITTCCHVDLKLKDFEYIYFSSCCLLF 278

OY 197 WTVFILMLVYVYVIAKRYDSYRSKSKDRKNKLEGVF--VVAVFVCFAPFHFA 253

DB 279 FVPIITTCYIGI-----IRLSSSSIENSCKKTRALFLAVVLCVFIFCGPTNLV 331

OY 254 RVPYTHSOTNNKTCRLQNLFIARETTLFLAATNICMDPLIYIFL--CKKTEKLPCM 310

DB 332 FLTHYLOEAN-----ELFYAYILSACVGSVSCCLDPLIYVYASSOCQRYLYSLCC 383

OY 311 Q-----GRKT-----TASSQENHSS 325

DB 384 RKVSEPGSGSTGOLMSTAMKNDNCST 408

RESULT 13

S44425

Angiotensin II receptor type 1 - dog

C:Species: Canis lupus familiaris (dog)

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Nov-1999

C:Accession: S44425

R:Burns, L.; Clark, K.L.; Bradley, J.; Robertson, M.J.; Clark, A.J.L. FEBS Lett. 343, 146-150, 1994

A:Title: Molecular cloning of the canine angiotensin II receptor. An AT1-like receptor w

A:Reference number: S44425; MUID:94222188

A:Accession: S44425

A:Status: nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-359 <BUR>

A:Cross-references: PIDN:AB30674.1; PID:9546569

A:Experimental source: liver

C:Superfamily: vertebrate rhodopsin

Query Match

17.2%; Score 298; DB 2; Length 359;

Best Local Similarity 26.3%; Pred. No. 2.5e-18;

Matches 89; Conservative 69; Mismatches 156; Indels 24; Gaps 10;

OY 1 MNTVMQGFNR-SERCPDRTR-IVQIVFPALYTVVLTGILNLT-ALWVFIHPPSSST 56

DB 3 LNSTEDGIRKIQDDCPKAGRMHYIFVMIPTLYSIIFVVGIFGNSLVIVIVYFMKLKTV 62

OY 57 FIYLNKNTLVADLIMTLMPFKILSDSHLAPWOLRAVCRSSVIFETMYGVILGLI 116

DB 63 ASVFLNLALADLCFLTLPLMAVVTAMEYRWPFPGNYLCKIASASVSFNLVYASFLLTCL 122

OY 117 AFDRFLKIIRPLRNIFLKKPVFAKTVSIFWFFLEFISLPMILSNK---EATPSSVKKC 173

DB 123 SIDRYVAIVHPKSPVRRTMLAKVTCIITWLAGLASIPTIIRNVFIENT--NITVC 180

OY 174 A-----SLKGPLGLKHWQVNNICQFIFWTVFILMLVYVYVIAKRYDSYRSKSKDRK 227

DB 181 AFHYESONSTPIGL--GLTKNIGLFL--PFLIITSYTLIWKTLKRAYEIQKNR- 234

OY 228 NNKKLEGVFVVAVFCFAPEHFAVVPYTHSQTNKTCRLQNLFIARETTLFLAAT 287

DB 235 -NDIIFKIIMAVLFFFSWVPHQIFTEFLDVLQLGIHDCIKIADIVDTAMPITICIAF 293

OY 288 NICMDPLIYIFLCKRFTKLPCKMOGRKTTASSQENHSS 325

DB 294 NNCLNPLFYGLGKFF--KKYFLQLLKIYPPKAKSHSS 329

RESULT 14

JC2134

angiotensin II receptor type 1A - rat

N:Alternate names: AT1a receptor; AT3 receptor

C:Species: Rattus norvegicus (Norway rat)

C:Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 24-Nov-1999

C:Accession: JC2134; S15404; S20424; JQ1055

R:Conchon, S.; Monnot, C.; Strleix, M.E.; Blhoreau, C.; Corvol, P.; Clauser, E. Biochem. Biophys. Res. Commun. 199, 1347-1354, 1994

A:Title: Synthetic cDNA encoding the rat AT1a receptor: a useful tool for structure-f

A:Reference number: JC2134; MUID:94197726

A:Accession: JC2134

A:Molecule type: mRNA

A:Residues: 1-359 <CON>

A:Note: the amino acid sequence of this protein is not given

R:Murphy, T.J.; Alexander, R.W.; Griendling, K.K.; Runge, M.S.; Bernstein, K.E. Nature 351, 233-236, 1991

A:Title: Isolation of a cDNA encoding the vascular type-1 angiotensin II receptor.

A:Reference number: S15404; MUID:91251901

A:Accession: S15404

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <MUR>

A:Cross-references: GB:X62295; NID:957773; PIDN:CAA44183.1; PID:9577774

R:Iwai, N.; Inagami, T. FEBS Lett. 298, 257-260, 1992

A:Title: Identification of two subtypes in the rat type I angiotensin II receptor.

A:Reference number: S20423; MUID:92183879

A:Accession: S20424

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-359 <IWA>

R:Iwai, N.; Yamano, Y.; Chaki, S.; Konishi, F.; Bardhan, S.; Tibbetts, C.; Sasaki, K. Biochem. Biophys. Res. Commun. 177, 299-304, 1991

A:Title: Rat angiotensin II receptor: cDNA sequence and regulation of the gene expres

A:Reference number: JQ1055; MUID:91254291

A:Accession: JQ1055

A:Molecule type: mRNA

A:Residues: 1-80, 'C', 82-108, 'T', 110-359 <IW2>

A:Cross-references: GB:M74054; NID:9202918; PIDN:AAA40738.1; PID:9202919

A:Experimental source: kidney

C:Comment: AT1 receptor consists of two closely related AT1 isoforms of angiotensin I

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; GTP binding; receptor; transmem

F:27-86/Domain: transmembrane #status predicted <TM1>

F:103-123/Domain: transmembrane #status predicted <TM3>

F:147-167/Domain: transmembrane #status predicted <TM4>

F:195-218/Domain: transmembrane #status predicted <TM5>

F:240-263/Domain: transmembrane #status predicted <TM6>

F:278-299/Domain: transmembrane #status predicted <TM7>

F:4,176,188/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

17.2%; Score 297; DB 2; Length 359;

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 11, 2002, 14:47:00 ; Search time 30 Seconds

(without alignments)
1920.244 Million cell updates/sec

Title: US-09-924-125-2

Perfect score: 1731
Sequence: 1 MNTTVMQGFNRSEKCPDRTR.....KTTASSQENHSSQTDNITLG 333

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

otal number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_19:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-rvivirus:*
- 16: sp-bacteriophage:*
- 17: sp-archaeal:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1731	100.0	333	4	Q9BPV8
2	1366	78.9	337	11	Q9D812
3	1128	65.2	228	6	Q9BE53
4	928	53.6	176	4	Q9BY61
5	833	48.1	342	6	Q9SKC3
6	830	47.9	342	6	Q9BGT8
7	829	47.9	342	4	Q9H244
8	813	47.0	347	11	Q9CPV9
9	807	46.6	343	11	Q9EPX4
10	767.5	44.3	338	11	Q9ESG6
11	692.5	40.0	358	4	Q9BY21
12	692.5	40.0	358	4	Q9BJZ8
13	681.5	39.4	359	11	Q99MT7
14	541.5	31.3	269	4	Q9BXC2
15	363.5	21.0	367	4	Q9UE21
16	339.5	19.6	337	4	Q9Y271

17	337.5	19.5	340	6	Q95N02	Q95N02 sus scrofa
18	331	19.1	342	6	Q9GK76	Q9GK76 capra hircu
19	330.5	19.1	298	4	Q9UDZ6	Q9UDZ6 homo sapien
20	326	18.8	342	6	Q9XSD4	Q9XSD4 sus scrofa
21	326	18.8	342	6	Q9TTY5	Q9TTY5 bos taurus
22	320.5	18.5	339	11	Q9J4T8	Q9J4T8 rattus norv
23	318.5	18.4	339	11	Q9J4T8	Q9J4T8 mus musculu
24	318.5	18.4	352	11	Q99J44	Q99J44 mus musculu
25	315.5	18.2	352	11	Q9JK47	Q9JK47 mus musculu
26	310.5	17.9	296	6	Q9TTY6	Q9TTY6 canis faml.
27	310.5	17.9	361	11	Q9JJS7	Q9JJS7 mus musculu
28	304.5	17.6	359	6	Q9N0U1	Q9N0U1 ovis aries
29	304	17.6	359	11	Q9EPP3	Q9EPP3 cavia porce
30	303.5	17.5	361	11	Q95811	Q95811 rattus norv
31	302	17.4	377	13	Q98U14	Q98U14 brachydantio
32	301.5	17.4	359	6	Q9GLN9	Q9GLN9 pan troglod
33	300	17.3	373	13	Q957585	Q957585 brachydantio
34	300	17.3	374	13	Q97466	Q97466 meleagris g
35	298	17.2	380	13	Q9DG06	Q9DG06 carassius a
36	295.5	17.1	360	6	Q9BG77	Q9BG77 pan troglod
37	293.5	17.0	361	13	Q90X57	Q90X57 xenopus lae
38	293	16.9	400	6	Q95M54	Q95M54 macaca fasc
39	292	16.9	454	4	Q9H573	Q9H573 homo sapien
40	290	16.8	362	11	Q9JLZ0	Q9JLZ0 rattus norv
41	290	16.8	362	11	Q91W10	Q91W10 mus musculu
42	289.5	16.7	383	13	Q42324	Q42324 catostomus
43	287	16.6	359	11	Q9EOR9	Q9EOR9 meriones un
44	287	16.6	400	6	Q9MYW9	Q9MYW9 macaca mula
45	286	16.5	393	11	Q9R1M0	Q9R1M0 mus musculu

ALIGNMENTS

RESULT 1

Q9BPV8 ID Q9BPV8 PRELIMINARY; PRT; 333 AA.

AC Q9BPV8; DT 01-JUN-2001 (TREMBLrel. 17, Created)

DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKSG77 (G-PROTEIN COUPLED RECEPTOR

DE GPR86) (G PROTEIN-COUPLED RECEPTOR) (G PROTEIN-COUPLED RECEPTOR

DE GPR86).

GN FKSG77 OR GPR86 OR GPR94.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=HEART;

RA Wang Y., Gong L.;

RT "Molecular cloning of FKSG77, a novel gene encoding a putative G-

RT protein-coupled receptor.";

RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21172992; PubMed=11273702;

RA Wittenberger T., Schaller H.C., Hellebrand S.;

RT "An expressed sequence tag (est) data mining strategy succeeding in

RT the discovery of new g-protein coupled receptors.";

RL J. Mol. Biol. 307:799-813(2001).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21458557; PubMed=11574155;

RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhitko O.,

RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;

RT "Discovery and mapping of ten novel G protein-coupled receptor

RT genes.";

RL Gene 275:83-91(2001).

RN [4]

RP SEQUENCE FROM N.A.

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RX PubMed-11546776;
RA Communi D., Gonzalez N.S., Detheux M., Brezillon S., Lannoy V.,
RA Parmentier M., Boeynaems J.M.;
RT "Identification of a Novel Human ADP Receptor Coupled to G1.";
RL J. Biol. Chem. 276:41479-41485(2001).
DR EMBL; AF345565; AAK29068.1; -
DR EMBL; AF295368; AAK01864.1; -
DR EMBL; AF411113; AAL26484.1; -
DR EMBL; AF406692; AAL01038.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KM Receptor.
SQ SEQUENCE 333 AA; 38440 MW; F234ABB50016DF34 CRC64;

Query Match 100.0%; Score 1731; DB 4; Length 333;
Best Local Similarity 100.0%; Pred. No. 7.8e-147;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNTVMQGFNRSECRPDRIVQVLVLPALYTVFLLTGILLNTLALWVFVHIPSSSTFIY 60
DB 1 MNTVMQGFNRSECRPDRIVQVLVLPALYTVFLLTGILLNTLALWVFVHIPSSSTFIY 60
QY 61 LKNTLVADLIMTLMPKILSDSHLAPWQLRAVFCRSSVIFETMYVGVILGLIAFDR 120
DB 61 LKNTLVADLIMTLMPKILSDSHLAPWQLRAVFCRSSVIFETMYVGVILGLIAFDR 120
QY 121 FLKIIRPLRNIFLKKPVAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
DB 121 FLKIIRPLRNIFLKKPVAKTVSIFWFFLFISLPMILSNKEATPSSVKKCASLKGPL 180
QY 181 GLKWHOMVNNICQFIWTVFILMLVYVVIKAKVYDSYRSKSKDRKNNKKLEGKVEYV 240
DB 181 GLKWHOMVNNICQFIWTVFILMLVYVVIKAKVYDSYRSKSKDRKNNKKLEGKVEYV 240
QY 241 AVEFVCFAPHFARVPYTHSQTNNKTDCLRLQNLFIARETTLFLATNICMDPLIYIFLC 300
DB 241 AVEFVCFAPHFARVPYTHSQTNNKTDCLRLQNLFIARETTLFLATNICMDPLIYIFLC 300
QY 301 KKFEKLPKCMQGRKTTASSQENHSSQTDNITLG 333
DB 301 KKFEKLPKCMQGRKTTASSQENHSSQTDNITLG 333

RESULT 2
Q9DBI2 PRELIMINARY; PRT; 337 AA.
Q9DBI2;
Q9DBI2 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 2010001L06RIK PROTEIN.
GN GPR86 OR 2010001L06RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Glisic C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pescie G., Quackenbush J.,
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldairelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaudo M.F.,

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RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-Oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK008013; BAB25409.1; -.
DR MGD; MGI:1921441; Gpr86.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 337 AA; 38693 MW; 2C1A76FBF893D5EA CRC64;

Query Match 78.9%; Score 1366; DB 11; Length 337;
Best Local Similarity 77.5%; Pred. No. 3.1e-114;
Matches 259; Conservative 34; Mismatches 37; Indels 4; Gaps 3;

QY 1 MNTVMQGFNRSEPCPRDTRIVOLVPEPALYTVVFLTGILNTLALWVFIHPSSTFIIV 60
   :||| |||||:|||||: ||| ||||| |||||:|||||:
Db 5 INTGMOGFNKSEKSPRDTMTQLFVLYTVFLAGILNTVALWVFIHPSNSTFIIV 64

QY 61 LKNTLVADLIMTLMPFKILSDSHLAPWQLRAFCRSSVIFVETMYVGIVLLGLIAFDR 120
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 65 LKNTLVADLIMLMLPFKILSDSHLAPWQLRGFVCTLSSVVEYETMYVGIMLGLIAFDR 124

QY 121 FLKTIIRPLNIFLKKPVFAKTVSIFIMFELFISLPMILSNKREATPSSVKKKASLKGPL 180
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 125 FLKTIIRPKTFVKKTAFAKTVSISVWSLMFISLPMIL-NKEATPSSVKKKASLKSPL 183

QY 181 GLKWHQMVNNICQIFWTVFILMLVFYVVIKVVDSYRKSRSKDRKNNKKLEGVFVV 240
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 184 GLMWHQVYSHTCQLIFWAVFILMLFYAVITKKVYNSYRKRFRKDSR-HKRLEVKVFIVM 242

QY 241 AVFFVCFAPFHFARVPYTHSQTNKTKDCRLQNLFIKETTLELATNICMDPLIYIFLC 300
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 AVFFVCFAPLHFVRIPYTSQTNKTKDCRLQNLFIKAEATLELATNICMDPLIYIILC 302

QY 301 KFTTEKLPCMGRK--TTASSQENHSSQTDNITL 332
   |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||: |||||:
Db 303 KFTQKVPVCRWKGARTAGSSEDHSSQTDNITL 336

RESULT 3
Q9BE53 PRELIMINARY; PRT; 228 AA.
AC Q9BE53;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHETICAL PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OC NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL CORTEX;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
   libraries.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
EMBL; AB056816; BAB39342.1; -.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 228 AA; 26356 MW; 47907F5DBEEDD22C CRC64;

Query Match 65.2%; Score 1128; DB 6; Length 228;
Best Local Similarity 94.7%; Pred. No. 3.9e-93;
Matches 216; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

OY 106 MYGVIVLGLIAFDRLKIRPLRNIFLKKPVFAKTVSIFITWFFLISLPNMLSKEA 165
Db 1 MYGVIVLGLIAFDRLKIRPLRNIFLKKTVFAKTVSIFITWFFLISLPNMLSKEA 60
OY 166 TPSSVKKCASLKGPLGLKWHQVNNICQIFWTVFILMLVYVYIAKKVDSYRKSXSD 225
Db 61 TPSSVKKCASLKGPLGLKWHQVNNISQIFWTVFILMLVYVYIAKKVDSYRKSXSD 120
OY 226 RKNKKLEGKVFVVAVFVCFAPHFHARVPYTHSQTNNKTCRLQNLFIKETTFLA 285
Db 121 RKNKKLEGKVFVVAVFVCFAPHFHTRVPYTHSQTNNKTCRLQNLFIKETTFLA 180
JY 286 ATNICMDPLIYIFLCKKTEKLPQMGRTTASSQENHSQTDNITIG 333
Db 181 ATNICMDPLIYIFLCKKTEKLPQMGRTTASSQENHSQTDNITIG 228

RESULT 4
O9BY61 PRELIMINARY; PRT; 176 AA.
AC O9BY61; 176 AA.
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE PUTATIVE G PROTEIN-COUPLED RECEPTOR GPCR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Wan T., Cao X.;
RT "Molecular cloning of a probable G protein-coupled receptor with three
transmembrane domains."
RL Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178982; AKR18752.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_Rhodopsn.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor.
SQ SEQUENCE 176 AA; 20194 MW; 352FDA2EA70EF9AD CRC64;

Query Match 53.6%; Score 928; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 2.2e-75;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 158 MILSNKEATPSSVKKCASLKGPLGLKWHQVNNICQIFWTVFILMLVYVYIAKKVDS 217
Db 1 MILSNKEATPSSVKKCASLKGPLGLKWHQVNNICQIFWTVFILMLVYVYIAKKVDS 60
OY 218 YRKSXSKDRKNNKLEGKVFVVAVFVCFAPHFHARVPYTHSQTNNKTCRLQNLFI 277
Db 61 YRKSXSKDRKNNKLEGKVFVVAVFVCFAPHFHARVPYTHSQTNNKTCRLQNLFI 120
OY 278 KETTLFLAATNICMDPLIYIFLCKKTEKLPQMGRTTASSQENHSQTDNITIG 333
Db 121 KETTLFLAATNICMDPLIYIFLCKKTEKLPQMGRTTASSQENHSQTDNITIG 176

RESULT 5
O95KC3 PRELIMINARY; PRT; 342 AA.
AC O95KC3;
DT 01-DEC-2001 (Tremblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL.39.5 KDA PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-MEDULLA OBLOGATA;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB062981; BAB60747.1;
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 39479 MW; E93FC26BBF5EC4C CRC64;

Query Match 48.1%; Score 833; DB 6; Length 342;
Best Local Similarity 49.1%; Pred. No. 1.3e-66;
Matches 155; Conservative 57; Mismatches 102; Indels 2; Gaps 1;

OY 15 CPRDRIVOLVFPALYTVFELTGILNTLALWVFIHPPSSSTFIYLNKTLVADLIMTL 74
Db 17 CTRDYKIQVLEPLLYTVLFVGLTNSLAMRIEFQIRSKSNFIIFLKNTVISDLMLIT 76
OY 75 LPFKILSDSHLAPWQLRAVFCRFSSVIFETMYVGIYVLLGLIAFDRLKIRPLRNIFLK 134
Db 77 FPFKILSDAKLAGPLRTFVCQVTSVIFETMYISISIFGLITIDRYOKTRPFKTSNK 136
OY 135 KPVFAKTVSIFITWFFLISLPNMLSKEATPSSVKKCASLKGPLGLKWHQVNNICQ 194
Db 137 NLGAKILSVLIWAFMFLSLPNMILTNRRPRDKNVKCCSFLKSEFGLVWHEIVNYICQ 196
OY 195 IFWTVFILMLVYVYIAKKVDSYRKSXSKDRKNNKLEGKVFVVAVFVCFAPHFHAR 254
Db 197 IFWTVFILVIVCYTLITKELIYRIVTRGVGKVPKRVNVKVFIIIAVFICFVPHFAR 256
OY 255 VPTYHSQTNNKTCRLQNLFIKETTFLAATNICMDPLIYIFLCKKTEKLPQMG--G 312
Db 257 IPTYLSQTRDVFDCAAENTLFYVKESTLWLTSLNACLDPIYFELCKSFRLSLSMKCP 316
OY 313 RKTASSQENHSQTD 328
Db 317 NSATSQSQDNRRKKEQD 332

RESULT 6
O9BGT8 PRELIMINARY; PRT; 342 AA.
ID O9BGT8;
AC O9BGT8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE HYPOTHETICAL.39.5 KDA PROTEIN.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-FRONTAL LOBE LEFT;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
libraries."
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB056385; BAB33041.1;
DR InterPro; IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.


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DR PRINTS: PR00237; GPCRHHODPSN.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Hypothetical protein.
SQ SEQUENCE 342 AA; 39497 MW; 3D21BF987FC48599 CRC64;

Query Match 47.9%; Score 830; DB 6; Length 342;
Best Local Similarity 49.1%; Pred. No. 2.3e-66;
Matches 155; Conservative 56; Mismatches 103; Indels 2; Gaps 1;

QY 15 CPRDTRIVQLVFPALYTVVETLGLINTLALWVFVHIPSSSTFIYIKNTLVADLIMTL 74
DB 17 CTRDYKITQVLEPLLYTVLFEVGLITNSLAMRTFFQIRSKSNFIIFLKNVTISDLMLIT 76
QY 75 LPEKILSDSHLAPWOLRAFYCRFSSVIFYETMYGVILGLIAFDRLKIIRPLRNIFLK 134
DB 77 FPEKILSDAKLGTGRLRTEFCOVTSVIFYETMYISISFLGITFDYRQKTRPEKTSNPK 136
QY 135 KPEVAKTVSIFWTFELFESISPMILSNKEATPSSVKKCASLKGPLGLKWHOMVNNICQF 194
DB 137 NLGAKILSVLIWAFMFLSLPMILTNRRPRDKKNVKKCSFLKSEFGLWHEIYVICQV 196
QY 195 IFWTFEILMLVEYVVIARKKYDSYRKSCKDRKNNKKLEGKVEVVAVFVCEAFPHFAR 254
DB 197 IFWINEFLIVIVCYTLITFKELYSYVTRGVGKVPKRKVNKVFIIIAVEFICFVPHFAR 256
QY 255 VPYTHSQTNKTDICRLQNLQLEIAKETTLFLAATNICMDPLIYIFLCKKTEKLPCMQ--G 312
DB 257 IPYTLSTQTRDVFDCAAENILFYVKESTIMTLTSLNACLDPFIYFFLCKSFRLSLMLKCP 316
QY 313 RKTASSQENHSSQTD 328
DB 317 NSATSQSQDNRRKKEQD 332

RESULT 7
Q9H244 PRELIMINARY: PRT; 342 AA.
AC Q9H244;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE P2Y12 PLATELET ADP RECEPTOR (G-PROTEIN COUPLED RECEPTOR SP1999)
DE (GI-COUPLED ADP RECEPTOR HOKR3).
DE HOKR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiiridae; Homo.
OC NCB1_TaxID-9606;
OX
NY
[1]
SEQUENCE FROM N.A.
MEDLINE-21037966; Pubmed-11196645;
RA Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,
RA Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,
RA Conley P.B.;
RA "Identification of the Platelet ADP Receptor Targeted by
RA Antithrombotic Drugs.";
RA Nature 409:202-207(2001).
RL
RN
[2]
SEQUENCE FROM N.A.
MEDLINE-21269433; Pubmed-11104774;
RA Zhang F.L., Luo L., Gustafson E., Lachowicz J., Smith M., Qiao X.,
RA Liu Y.-H., Chen G., Pramanik B., Laz T.M., Palmer K., Bayne M.,
RA Monsma F.J. Jr.;
RA "ADP is the cognate ligand for the orphan G protein-coupled receptor
RA SP1999.";
RL J. Biol. Chem. 276:8608-8615(2001).
RN
[3]
SEQUENCE FROM N.A.
MEDLINE-21394281; Pubmed-11502873;
RA Takasaki J., Kamohara M., Saito T., Matsumoto M., Matsumoto S.,
RA Ohishi T., Soga T., Matsushime H., Furulich K.,
RA "Molecular cloning of the platelet P2YAC ADP receptor.;"
RA Pharmacological comparison with another ADP receptor, the P2Y1

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Query Match	47.9%	Score 829;	DB 4;	Length 342;
Best Local Similarity	49.1%	Pred. No. 2.9e-66;		
Matches 155;	Conservative 57;	Mismatches 102;	Indels 2;	Gaps
QY 15	CPDRTRIVQLVFPALYTVFVLTGILLNTLALNVFVHIPSSSTFIILYKNTLVADLIMTLM 74			
DB 17	CTRDYKITOVLPPLLYTVLFVGLITNGLAMRIFFQIRSKSNFIIFLKNTVISDLIMLT 76			
QY 75	LPFKTSDSHLAPWQLRAFCVRCSSVIFETMTVGIVLLGLIAFDRLKIIRPLRNIFLK 134			
DB 77	FPEKILSDAKLGTGPLRTFVCQVTSVIFFTMYISISFLGLITIDRYOKTTRPEKTSNP 136			
QY 135	KPYEAKTVSIFIFWFFLFISLPMILSNKEATPSSVKKCASLKGPLGLKWHQVNNICOF 194			
DB 137	NLIGAKILSVIWAEMFLSLPMILTNQPRDKNVKKCSFLKSEGLVWHEIVNYICOV 196			
QY 195	IFWTFVFLMLVFYVVIKAVYDSYRKSQDKRNNKKLEGVFNVAVFVCFAPFHEAR 254			
DB 197	IFWTFVFLMLVICYTLITKELYSYVTRGVGRVPRKKVNVKVFIIIAVFICFVPEHFR 256			
QY 255	VPTHTSOTNNKTDRCRLQNLFIKETTFLIATNICMDPLIYIFLCKKFTTEKLPQMO--G 312			
DB 257	IPYTLSTQTRDVFDCETAENTLFYVKESTLWLSLNACLDPIFYEFFLCKSFRLNLSMLKCP 316			
QY 313	RKTASSQENHSSQTD 328			
DB 317	NSATSLSQDNRRKKEOD 332			
RESULT 8				
Q9CPV9	PRELIMINARY;	PRT;	347 AA.	
ID Q9CPV9;				
AC Q9CPV9;				
AD Q9CPV9;				
DT 01-JUN-2001 (TREMBLrel. 17, Created)				
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)				
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)				
DE 4921504D23RIK PROTEIN (2900079B22RIK PROTEIN).				
GN P2RY12 OR 4921504D23RIK OR 2900079B22RIK.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX NCBI_TaxID=10090;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC STRAIN=C57BL/6J; TISSUE=TESTIS, AND HIPPOCAMPUS;				
RX MEDLINE=21085660; PubMed=11217851;				
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,				
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,				
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,				
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,				
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Nombaerts P.,				
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				

RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Wittlaker C., Wilming L.,
RA Wnshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL; AK014807; BAB29561.1; -.
DR EMBL; AK013804; BAB29000.1; -.
DR MGD; MGI:1918089; P2ry12.
DR MGD; MGI:1920308; 2900079B22Rik.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
SQ SEQUENCE 347 AA; 39473 MW; F107488E57E025F1 CRC64;

Query Match	47.0%;	Score 813;	DB 11;	Length 347;
Best Local Similarity	47.8%;	Pred. No. 7.8e-65;		
Matches 155;	Conservative 56;	Mismatches 107;	Indels 6;	Gaps 22;

[illegible]

RESULT	9		
Q9EPX4			
ID	Q9EPX4	PRELIMINARY;	PRT; 343 AA.
AC	Q9EPX4;		
DT	01-MAR-2001 (TREMBLrel. 16, Created)		
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
DE	P2Y12 PLATELET ADP RECEPTOR.		
OS	Rattus norvegicus (Rat).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
OX	NCBI_TaxID=10116;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-SPRAGUE-DAWLEY;		
RX	MEDLINE-21037966; PubMed-11196645;		
RA	Hollopeter G., Jantzen H.-M., Vincent D., Li G., England L.,		
RA	Ramakrishnan V., Yang R.-B., Nurdan P., Nurdan A., Julius D.J.,		
RA	Conley P.B.;		
RT	"Identification of the Platelet ADP Receptor Targeted by		
RT	Antithrombotic Drugs.";		
RL	Nature 409:202-207(2001).		
DR	EMBL; AF313450; AAG48945.1; -		
DR	InterPro; IPR000276; GPCR_Rhodpsn.		
DR	Pfam; PF00001; 7tm_1; 1.		
DR	PRINTS; PR00237; GPCR_RHODOPSN.		
DR	PROSITE; PSS0262; G_PROTEIN_RECPT_F1_2; 1.		
KW	Receptor.		
SO	SEQUENCE 343 AA; 39047 MW; 7AE0AFCE66674136 CRC64;		

Query Match	46.6%;	Score 807;	DB 11;	Length 343;
Best Local Similarity	47.2%;	Pred. No. 2.6e-64;		
Matches 151;	Conservative 60;	Mismatches 107;	Indels 2;	Gaps 1;

[illegible]

RESULT 10

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ID Q9ESG6 PRELIMINARY; PRT; 338 AA.
AC Q9ESG6;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE 7 TRANSMEMBRANE G-PROTEIN COUPLED RECEPTOR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Lee B.C., Scadden D.T.;
RT "7 transmembrane G protein coupled receptor from hematopoietic
RT progenitors.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF177211; AAC09275.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR RHODOPSIN.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; Transmembrane.
SQ SEQUENCE 338 AA; 38861 MW; 4376B50622A68A4E CRC64;

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Query Match	44.3%;	Score 767.5;	DB 11;	Length 338;
Best Local Similarity	43.2%;	Pred. No. 8.8e-61;		
Matches 142; Conservative	64;	Mismatches 112;	Indels 11;	Gaps 3

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QY 12 SERCPDRIVOLVLPALTYVELTGILLNTLALWVEVHPSSSTFIYLYKNTLVADLM 71
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 NOPCSNNTLITKOIIPVLYGMVFTITGLLLNGISGWIFFEYVPSKSPFIYLYKNIVADFLM 70
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 72 TLMPEFKILSDSHLAPWOLRAFCVCRFSSVIEYETMYGIVLGLIAFDRELKIIRPLRNI 131
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 GLTFEPFKVLGDSGLGPMQVNVFVCRAVSAVIEFYVMYVSIVIEFGLISFDRYKKIVKPLITS 130
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 FLKKPVEAKTVSIFIEWFELEFISLPMILSNKEATPSSVYKCASLGKPLGKWHOMVNNI 191
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 IVOSVNYSKLLSVLWMMMLMLLAVPNIIILTNOGVKEVTKIQCMELKKNELGRKWHKASNYI 190
   :: : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 COFLFWTVFIIMLVEFYVVIARKVYDSYRKSCKDRKNKKEGKVEVVVAVFVYCFAPBH 251

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Db 191 FVSIWFVFLLLIVFYTAITRKIFKSHLKSRSKNSTSVKRSKSSRNIFSIYLVFVYCEVPYH 250
OY 252 FARVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIFLCKKFTF----- 305
Db 251 IARIPYKTSQTEGHYSCRTKETLLYAKFETLLSAAVCLDPIIYFELCQPFREVLNKKL 310
OY 306 --KLPCMGRKKTASSQEN--HSSQTDNI 330
Db 311 HMSLKVQNDLEVSQKTKRENAIHES-TDTL 338

RESULT 11
ID 09BY21 PRELIMINARY; PRT; 358 AA.
AC 09BY21;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE ORPHAN G PROTEIN-COUPLED RECEPTOR 87.
GN GPR87 OR GPR95.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-21172992; PubMed-11273702;
RA Wittenberger T., Schaller H.C., Hellebrand S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new g-protein coupled receptors."
RL J. Mol. Biol. 307:799-813(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-21458557; PubMed-11574155;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vantl W.B., Arkhltko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes."
RL Gene 275:83-91(2001).
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL; AF237763; AK01858.1; -
DR EMBL; AF411114; AAL26485.1; -
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEPTOR_F1_2; 1.
? G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
>Q SEQUENCE 358 AA; 41435 MW; FDF157295BE5D10F CRC64;

Query Match 40.0%; Score 692.5; DB 4; Length 358;
Best Local Similarity 41.0%; Pred. No. 4.6e-54;
Matches 125; Conservative 70; Mismatches 99; Indels 11; Gaps 3;

OY 10 NRSERCPRDTRIYQ---LVFPALYTVVFLGILLNTLALMVFVHIPSSSTFIYLNKTL 65
Db 25 NRSDDPGKNTTLHNEFDITVLPVLYLIIFVASILLNGLAWVIFHIRNKTSFIYLNKIV 84
OY 66 VADLIMTLMPFKILSDSHLAPWQRAVFCRSSVIFYETMVGIVLGLIAFDRLKII 125
Db 85 VADLIMTLTFPRIVHDAGFGPWYFKFICRYTSVLFYANMTSIVFLGLISIDRYLKVV 144
OY 126 RPLRNIFLKKPYFAKTVSIFIFWFLFISLPMILSNKEATISSVKKCASLKGPLGLKWH 185
Db 145 KPEGDSRMYSITFTKVLSCVWVIMAVLSLPIILLTGQPTIDNIHDCSKLSPGLVKWH 204
OY 186 QMVNNICQFIETVFIIMLVFYVVIKAVYDSYRK--SKSKDRKNNKLEGVVVAV 242
Db 205 TAVTYVNSCLFVAVLVILGCIYIAISRYIHKSSROFISQSSIKRKHQSIR---VVAV 260
OY 243 FVCFAPFHFAVVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIFLCKK 302
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Db 261 FETCFLPYHLCRIPFTFSHLDRLDESAQKILYCKEITTLFLSACNVCLDPIIYFEMCRS 320
OY 303 FTEKL 307
Db 321 FSRRL 325

RESULT 12
ID 096J28 PRELIMINARY; PRT; 358 AA.
AC 096J28;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CDNA FLJ14878 FIS, CLONE PLACE1003238, WEAKLY SIMILAR TO PROBABLE
DE G PROTEIN-COUPLED RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA;
RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shitatori A., Sudo H.,
RA Wagatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chida Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y.,
RA Minomiyu K., Iwayanagi T.;
RT "NEDO human cDNA sequencing project."
RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK027784; BAB55366.1; -
RL SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;
SQ SEQUENCE 358 AA; 41462 MW; 7822700C8E3CC7E9 CRC64;

Query Match 40.0%; Score 692.5; DB 4; Length 358;
Best Local Similarity 41.0%; Pred. No. 4.6e-54;
Matches 125; Conservative 70; Mismatches 99; Indels 11; Gaps 3;

OY 10 NRSERCPRDTRIYQ---LVFPALYTVVFLGILLNTLALMVFVHIPSSSTFIYLNKTL 65
Db 25 NRSDDPGKNTTLHNEFDITVLPVLYLIIFVASILLNGLAWVIFHIRNKTSFIYLNKIV 84
OY 66 VADLIMTLMPFKILSDSHLAPWQRAVFCRSSVIFYETMVGIVLGLIAFDRLKII 125
Db 85 VADLIMTLTFPRIVHDAGFGPWYFKFICRYTSVLFYANMTSIVFLGLISIDRYLKVV 144
OY 126 RPLRNIFLKKPYFAKTVSIFIFWFLFISLPMILSNKEATISSVKKCASLKGPLGLKWH 185
Db 145 KPEGDSRMYSITFTKVLSCVWVIMAVLSLPIILLTGQPTIDNIHDCSKLSPGLVKWH 204
OY 186 QMVNNICQFIETVFIIMLVFYVVIKAVYDSYRK--SKSKDRKNNKLEGVVVAV 242
Db 205 TAVTYVNSCLFVAVLVILGCIYIAISRYIHKSSROFISQSSIKRKHQSIR---VVAV 260
OY 243 FVCFAPFHFAVVPYTHSQTNNKTDCLONOLFIAKETTLFLAATNICMDPLIYIFLCKK 302
Db 261 FETCFLPYHLCRIPFTFSHLDRLDESAQKILYCKEITTLFLSACNVCLDPIIYFEMCRS 320
OY 303 FTEKL 307
Db 321 FSRRL 325

RESULT 13
ID 099MT7 PRELIMINARY; PRT; 359 AA.
AC 099MT7;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE G-PROTEIN COUPLED RECEPTOR GPR87.
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GN GPR87.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-21172992; PubMed-11273702;
RX Wittenberger T., Schaller H.C., Hellebrend S.;
RT "An expressed sequence tag (est) data mining strategy succeeding in
RT the discovery of new g-protein coupled receptors.";
RL J. Mol. Biol. 307:799-813(2001).
CC -! SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF295366; AAK01866.1; -.
DR MGD; MGI:1934133; Gpr87.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1; 1.
DR PRINTS; PR00237; GPCRRHODOPSN.
JR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
JR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 359 AA; 41462 MW; 2EB313C273EFCDEA CRC64;

Query Match          39.4%; Score 681.5; DB 11; Length 359;
Best Local Similarity 42.2%; Pred. No. 4.4e-53;
Matches 121; Conservative 62; Mismatches 97; Indels 7; Gaps 2;

OY 24 LVFPALTYVFLTGILNTLALMVFHIPSSSTFIYLKNTLVADLTMTLMPEKILSDS 83
   ::|||::|: |||||::|: | : :||| ||||| |||::|:
Db 44 ILPLVLTVIVFASILLNGLAVWIFPHIRNKTSFIFYLKNIYVADLTMTLTPEFRIVRDA 103

OY 84 HLAPWQLRAFVCRESSVIFETMYVGIVLGLIAFDRLKIIRPLRIELKKPVFAKTVS 143
   || ::::|::| | | | ||||: |::|: | : | :|
Db 104 GFGEPMYFEFILCRYTSLVFAYNMYSIVFGLISVDRLKYVKPFQDSRMYSITFTKVL 163

OY 144 IFIWFLEFFISLPNMI LSNEATPPSSVKKCASLKGPIGLKHWQMNNICQIFIWTFEILM 203
   ::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 164 VCVWVMAILSLPNII LITNGOPTKENIHDCMKLSPLGAKHMMAVTYVDSCLFVAVLVIL 223

OY 204 LVFYVVI AKKVYDSYRK---SKSKDRKNKKLEGVVVVAVFVCFAPFHFAVPYTHS 260
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 224 IGCYIAISR YIHKSSROFISOSSSRKRKHQSIR---VYVAVFTCTPLPYHLCRIPFTFS 279

OY 261 QTNNKTDCLRLOQLFAKETTLFLAATNICMDPLIYIFLCKKETEKL 307
   :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 280 NLDRLLDESAHKILYYCKEMTLFLSACNVCLDPIYEFWMCKSFSSRRU 326

RESULT 14
O9BXC2 PRELIMINARY; PRT; 269 AA.
AC O9BXC2;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PUTATIVE G-PROTEIN-COUPLED RECEPTOR FKS678 (G PROTEIN-COUPLED RECEPTOR
DE 87).
GN FKS678.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=HEART;
RA Wang Y.-g, Gong L.;
RT "Identification of fks678, a novel gene encoding a putative G-protein-
RT coupled receptor.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
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RA Strausberg R.;
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR EMBL: AF345566; AAK29069.1; -.
DR EMBL: BC009540; AAH09540.1; -.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Glycoprotein; Receptor; Transmembrane.
SQ SEQUENCE 269 AA; 3143 MW; 1E7D498EE20717F6 CRC64;

Query Match 31.3%; Score 541.5; DB 4; Length 269;
Best Local Similarity 39.6%; Pred. No. 1.1e-40;
Matches 95; Conservative 56; Mismatches 82; Indels 7; Gaps

QY 71 MTLMLPEKILSDSHLAPWQLRAVFCRFSVIFYETMYVGIVLGLIAPDRFLKIIRPLRN 130C
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
Db 1 MTLTFEPRIVHDAGFGPMWFKFILCRYTSVLYFANMTSTIVFGLISIDRYLKVPKPGD 60

QY 131 IFLKRPVFAKTVSIFIMFELFISLPMNLSNKEATPSSVKKCASLKGPIGLKWHQWVNN 190C
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 61 SRMYSITFTKVLSCVMVIMAVLSLPNITLNGOPTEDNIHDCSKLSPGVKWHTAVTY 120C

QY 191 ICQFIWTVFELMLVEYVVIKAKVYDSYR---SKSKDRKNKKEGKVFVVAVVAVFVCF 247C
   : :| : : : : : : : : : : : : : : : : : : : : : : : :
Db 121 VNSCLFVAVLVILGICCYIAISRYIHKSSKROFISQSSRRKKHNSIR---VVAVVFYTCF 176C

QY 248 APFHFAVPVPTHSQTNKKTDCRLQNLFIKETTFLAATNICMDPLIYIFLCKKFTTEKL 307C
   ||| ||| : : : : : : : : : : : : : : : : : : : : : : :
Db 177 LPYHLCRIPEFTSHLDRLDESAOKILYCKEITLFLSACNVCIDPIIYFFMCRSFSSRL 236C

RESULT 15
Q9UE21 PRELIMINARY; PRT; 367 AA.
AC Q9UE21;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE P2Y-LIKE G-PROTEIN COUPLED RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID-9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Blasius R.H., Weber R.G., Lichter P., Ogilvie A.;
RT "A novel orphan G-protein coupled receptor primarily expressed in the
RT brain is localized on human chromosomal band 2q21.";
RL J. Neurochem. 1998;1357-1365(1998).
DR EMBL: Y12546; CAA73144.1; -.
DR HSSP; P34996; 1DDO.
DR InterPro: IPR000276; GPCR_Rhodpsn.
DR Pfam: PF00001; 7tm_1; 1.
DR PRINTS: PR00237; GPCR_Rhodopsn.
DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; UNKNOWN_1.
DR PROSITE: PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Receptor; G-protein coupled receptor.
SQ SEQUENCE 367 AA; 40989 MW; 132FBE97BE8360C CRC64;

Query Match 21.0%; Score 363.5; DB 4; Length 367;
Best Local Similarity 27.7%; Pred. No. 1.1e-24;
Matches 90; Conservative 69; Mismatches 137; Indels 29; Gaps

QY 12 SERCPDRIVQLVFPALYTVVFLTGILLNTLALWVFVHIPSSST-FIYLKNTLVADLI 70
   :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
Db 48 AEQCGQETPLENMLFASFYLLDFILALVGNLTALWLFIRDHKSGTPRANVFIMHLAVADLS 107

QY 71 MTLMLPEKIL---SDSHLAPWQLRAVFCRFSVIFYETMYVGIVLGLIAPDRFLKIIRP 127
   ||| ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :

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Db      108  CVLVLPRLVYHFGSNH--WPEGEIACRLTGFLFYLNMYASIFYELTICISADRFIAIVHP 164

.QY     128  LRNIFLKKPVEAKTVSIFIFWEFLFISLPMILSNKEATPSSVKKCASLKGPLGLKWHQM 187
      ::: |:|::| |:|: ::: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|:
Db      165  VKSLKLRRLPYAHLACAFWM-VVAVAVAMAPLVSQTVQTNHIVVCQLYREKA-SHHAL 222

.QY     188  VNNICOFIEWTVEFILMLVEYVVIACKVYDSYRKSksKDRKNNKKLEGKEVVVAVVEVCF 247
      |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|:
Db      223  VSLAVAFITF--PITTVTCYLLIIR---SLRQGLRVEKRLKTKAVRMAIYALIFVCF 276

.QY     248  APFHFARVPTYHSQTNKTDCLRONOLFIAKETTLFLAATNICMDPLIYIFLCKKFEKL 307
      |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|: |:|:
Db      277  VPHYHVNRSYVVLHYRSHGASCACQRIALANRITSCLTSLNGALDPIMYFVAEKERHAL 336

.QY     308  -----PCMGRKRTASS 319

Db      337  CNLIGKRLKGPPSPFEG-KTNESS 360

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Search completed: October 11, 2002, 14:49:49
Job time : 31 secs